HUMAN xiap

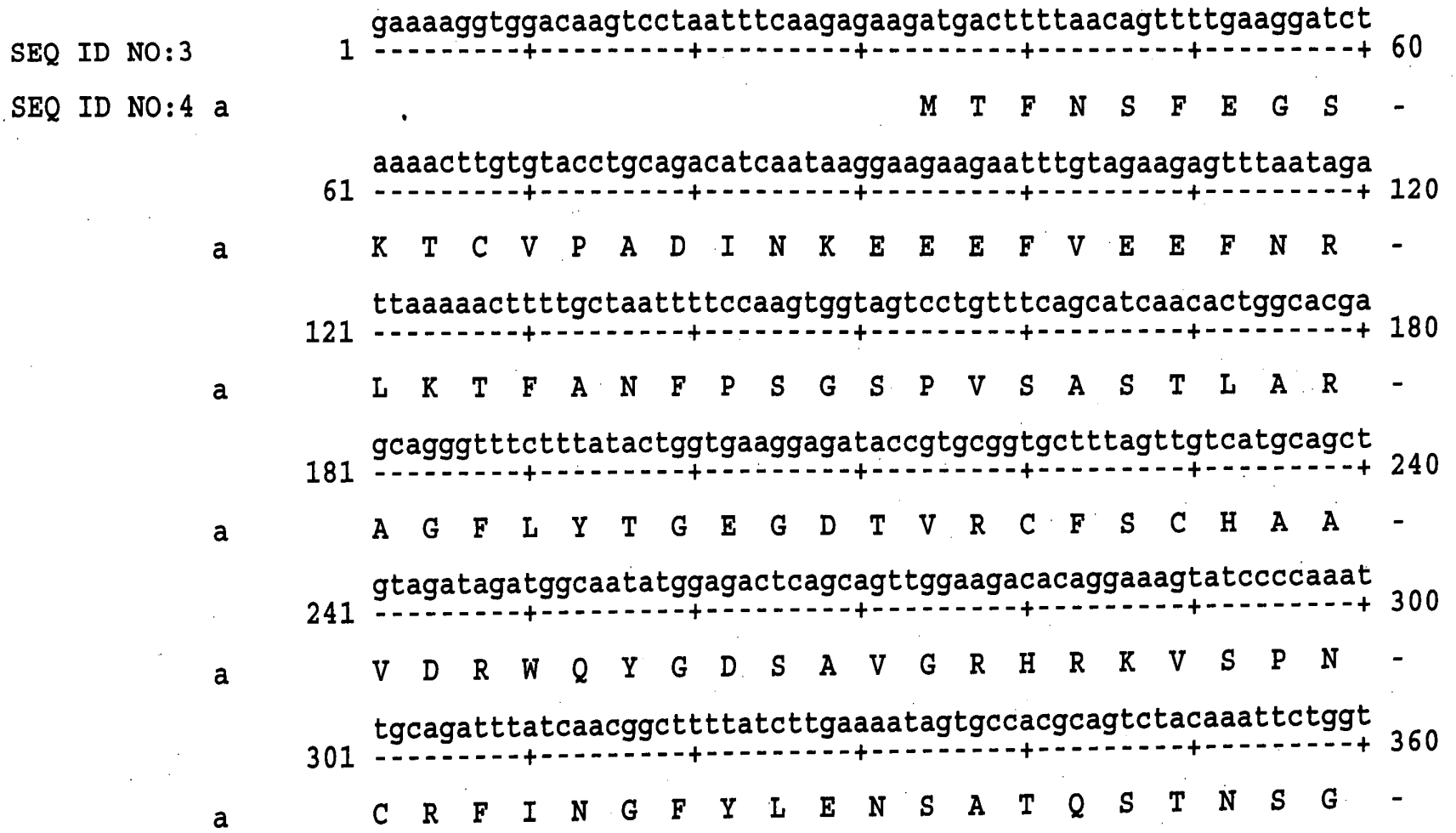

Fig. 1 (page 1 of 7)

HUMAN xiap

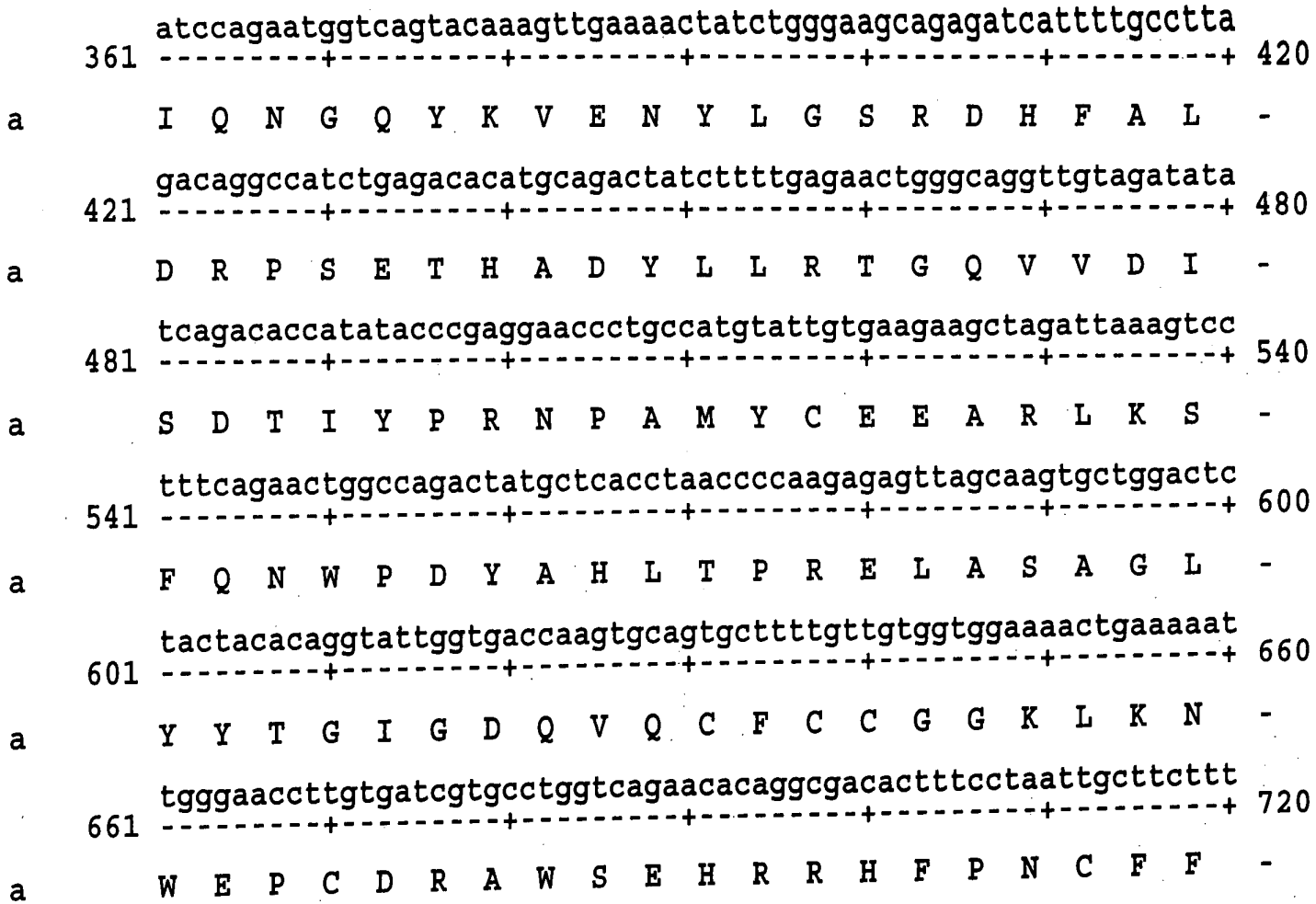

Fig. 1 (page 2 of 7)

HUMAN xiap

Fig. 1 (page 3 of 7)

HUMAN xiap

Fig. 1 (page 4 of 7)

HUMAN xiap

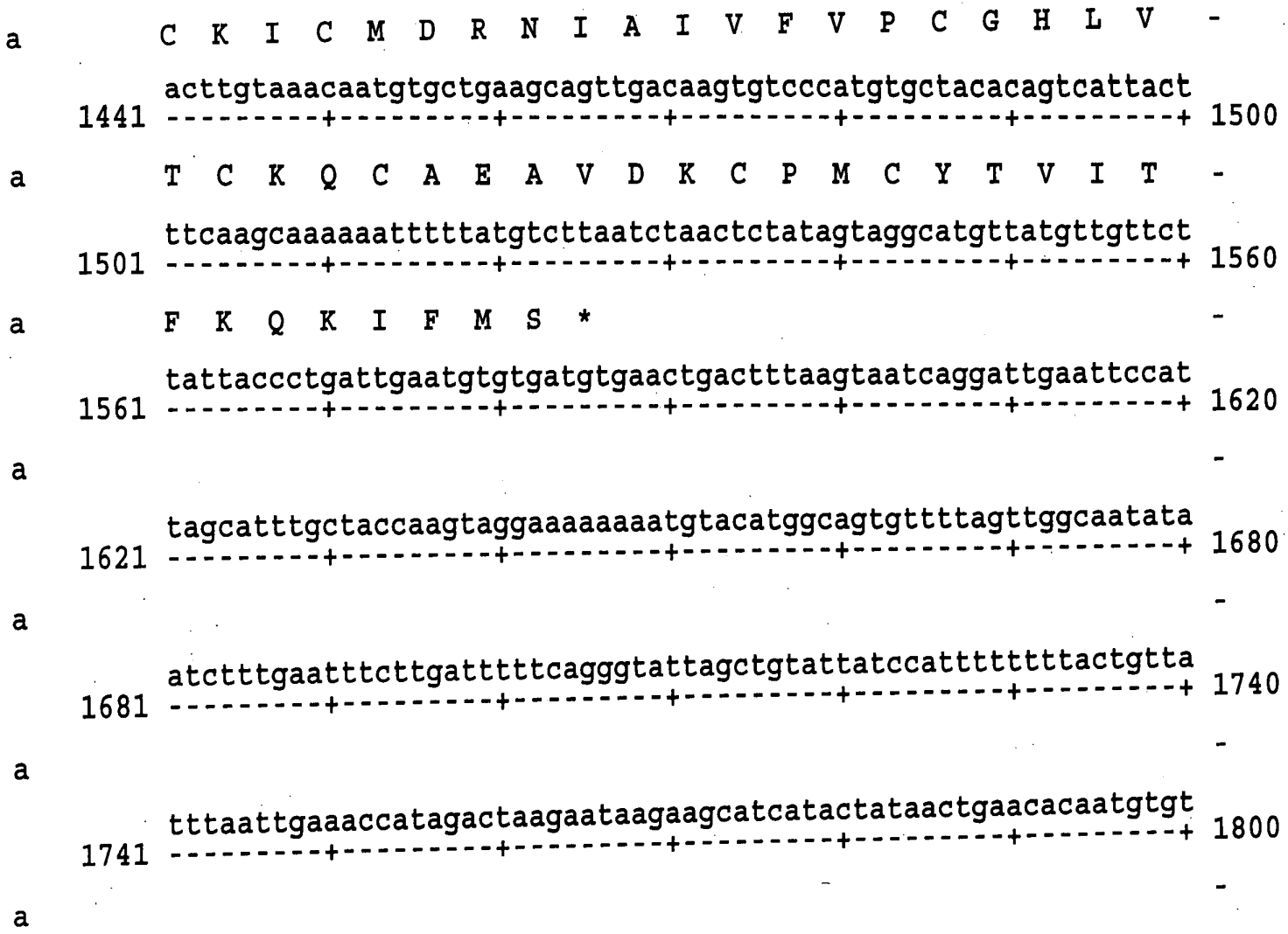

Fig. 1 (page 5 of 7)

HUMAN xiap

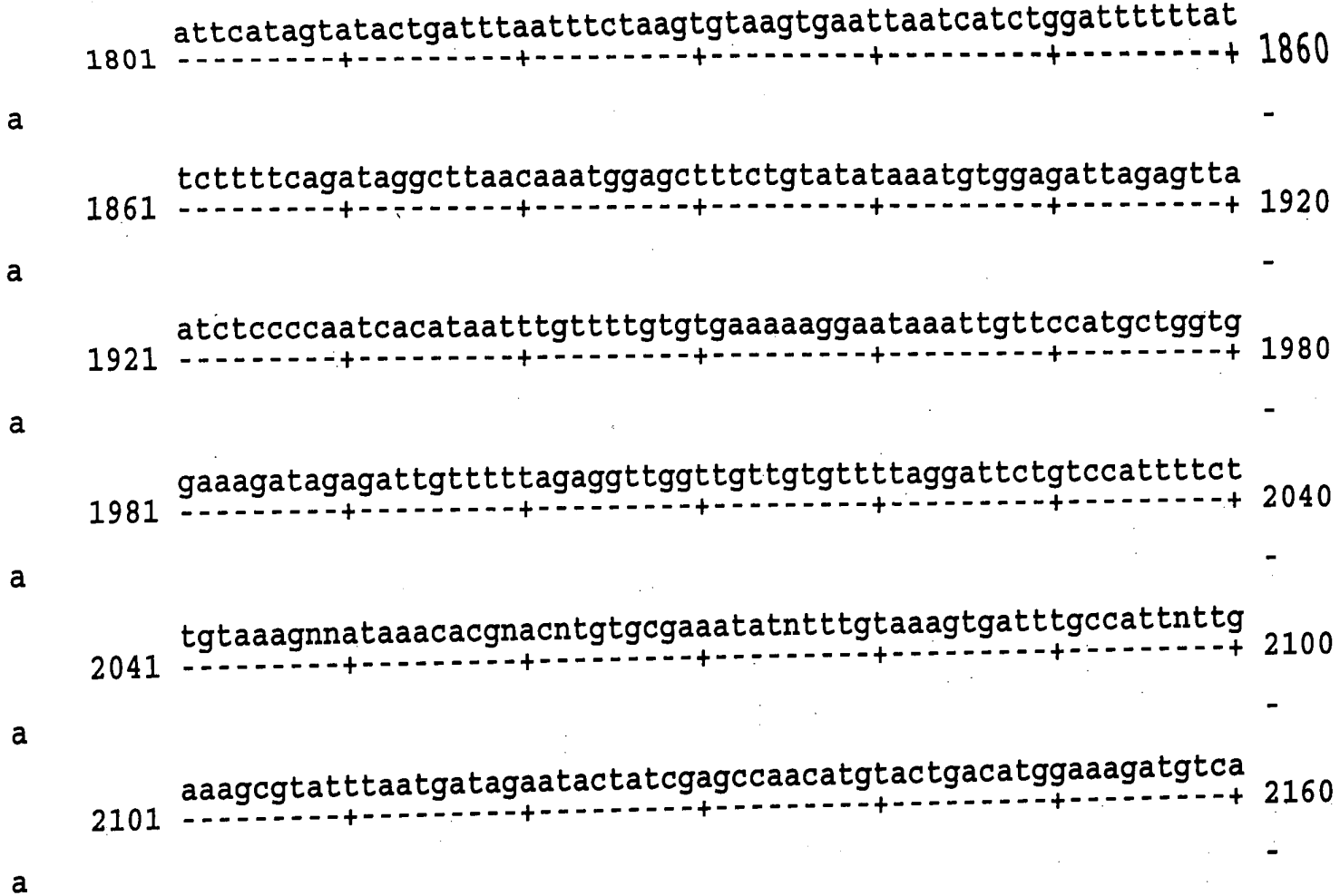

Fig. 1 (page 6 of 7)

HUMAN xiap

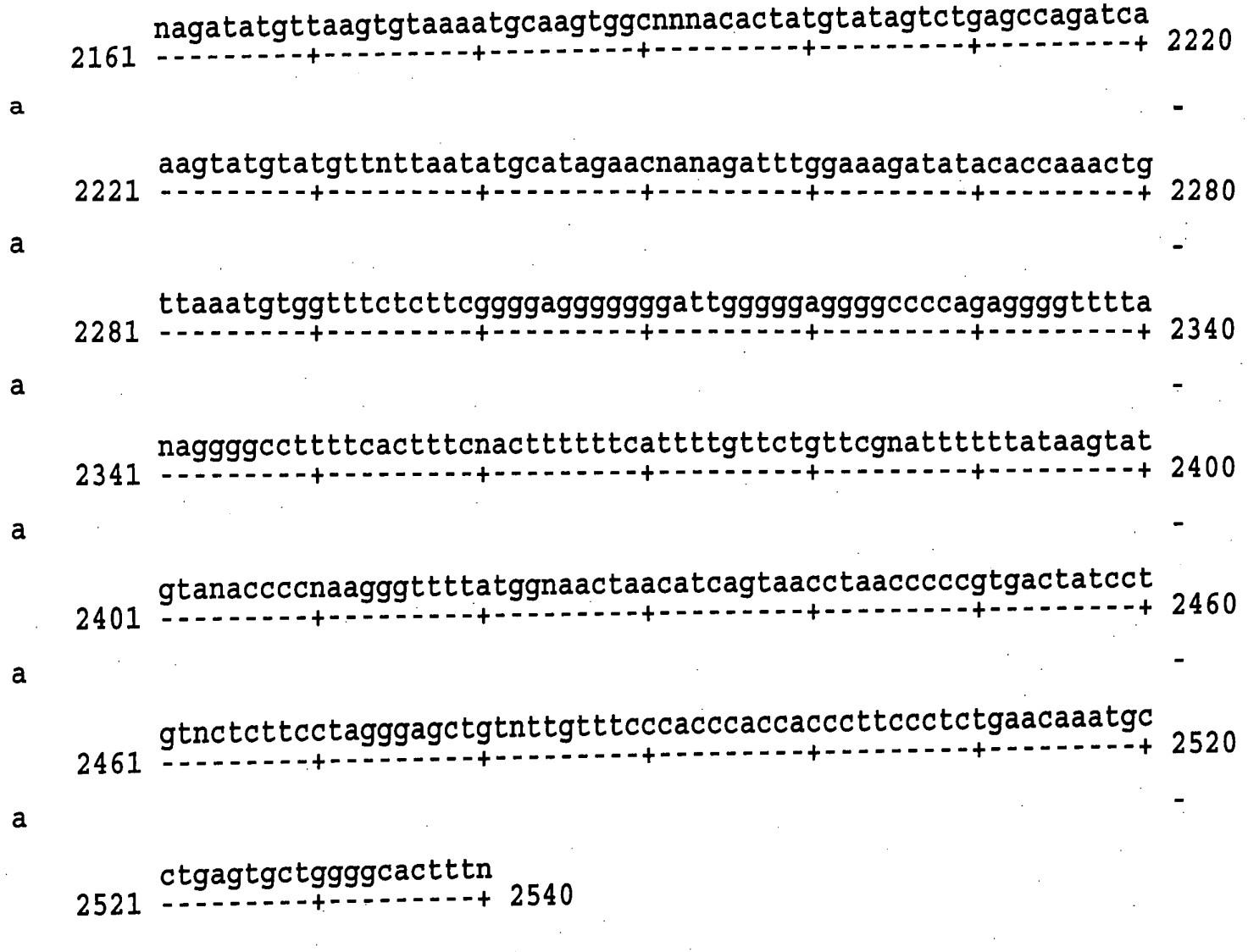

Fig. 1 (page 7 of 7)

HUMAN hiap-1

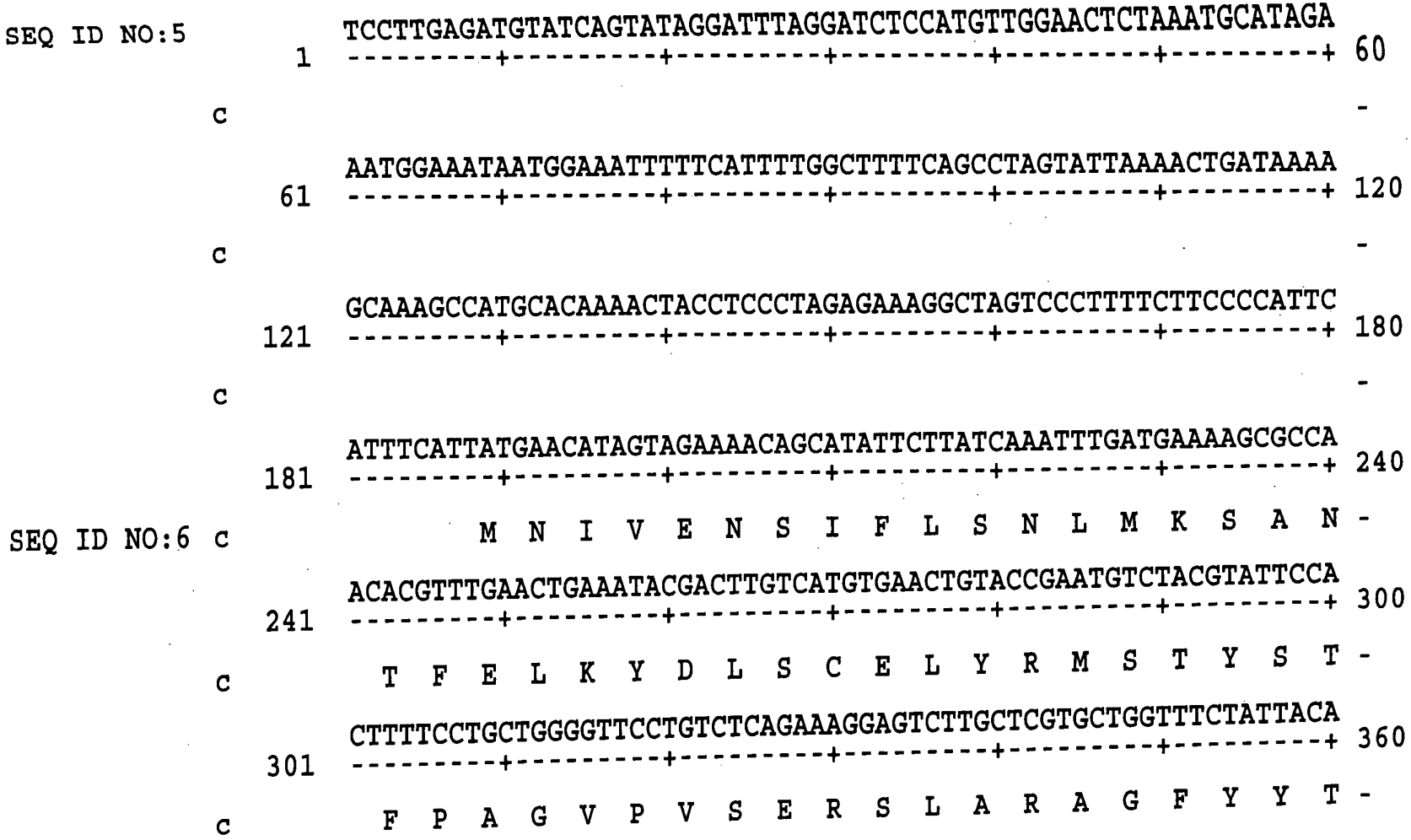

Fig. 2 (page 1 of 8)

HUMAN hiap-1

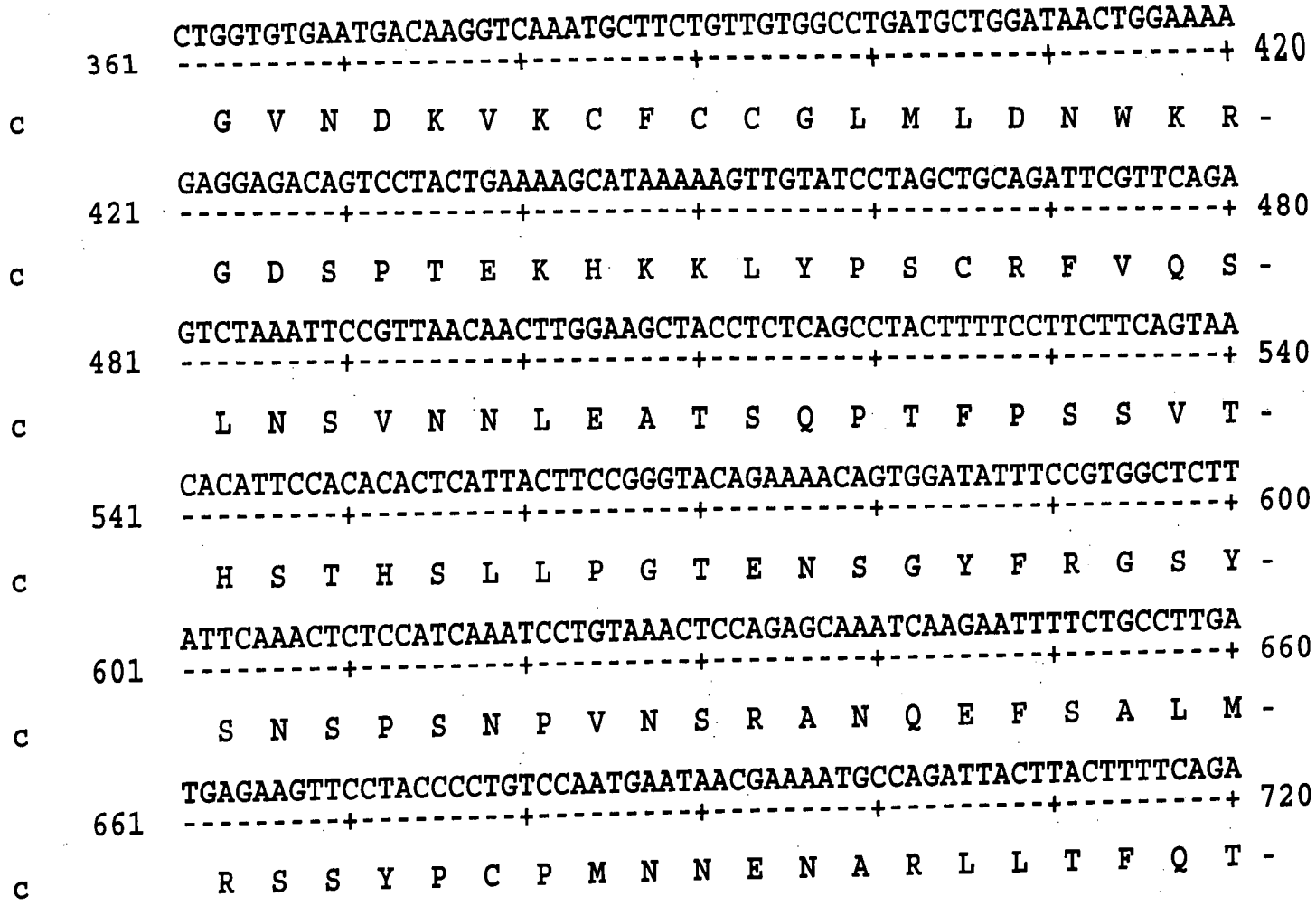

Fig. 2 (page 2 of 8)

HUMAN hiap-1

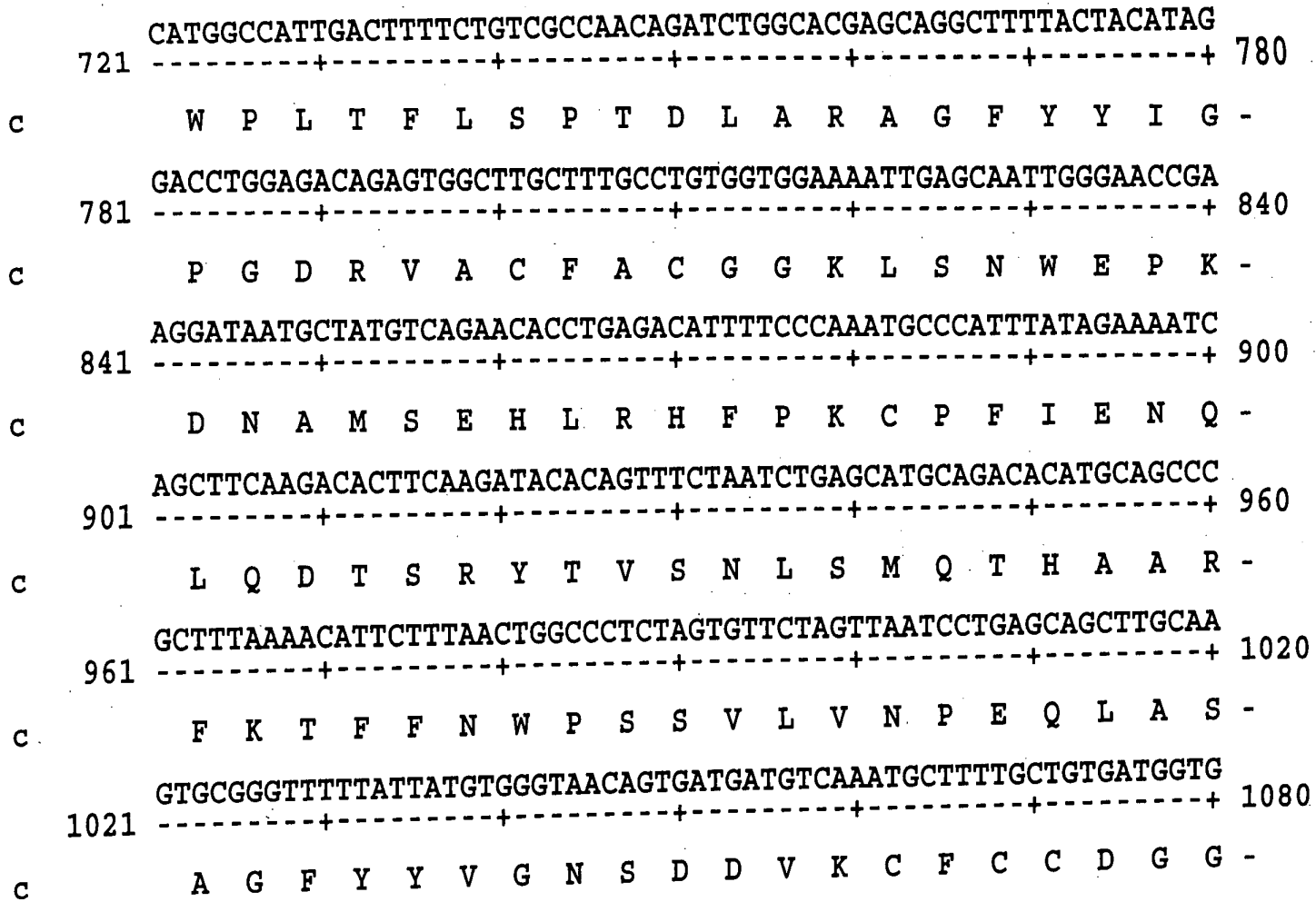

Fig. 2 (page 3 of 8)

HUMAN hiap-1

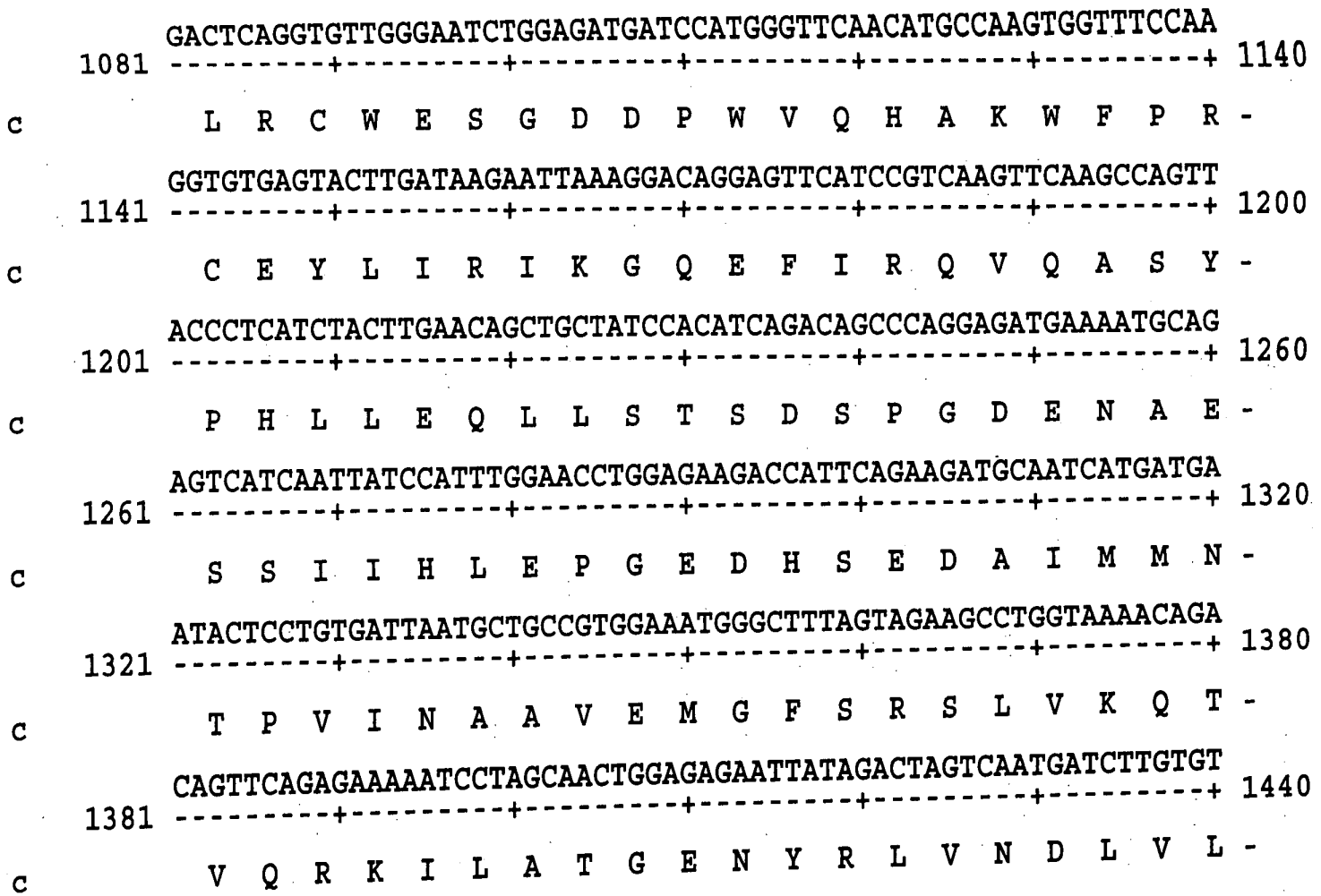

Fig. 2 (page 4 of 8)

HUMAN hiap-1

Fig. 2 (page 5 of 8)

HUMAN hiap-1

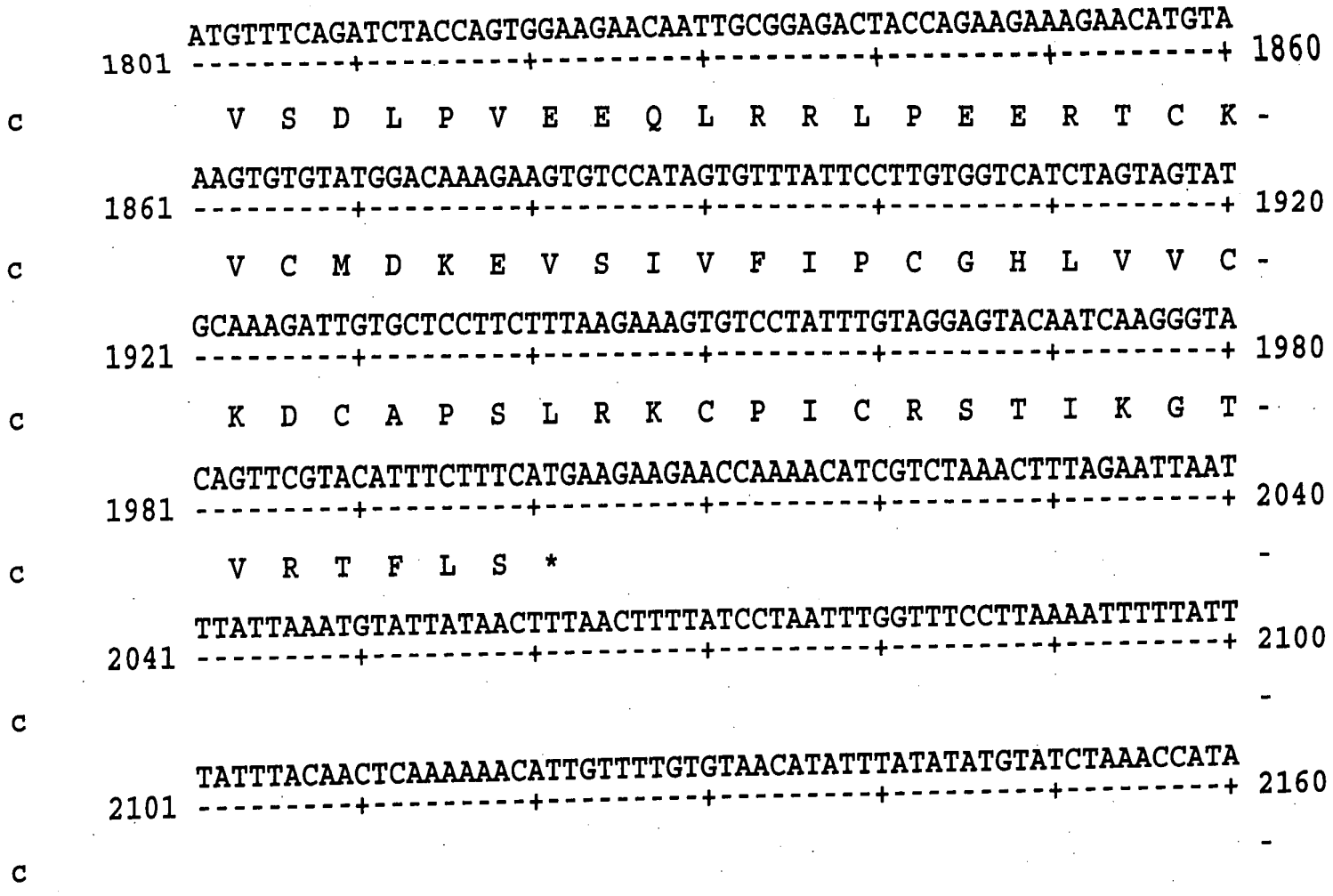

Fig. 2 (page 6 of 8)

HUMAN hiap-1

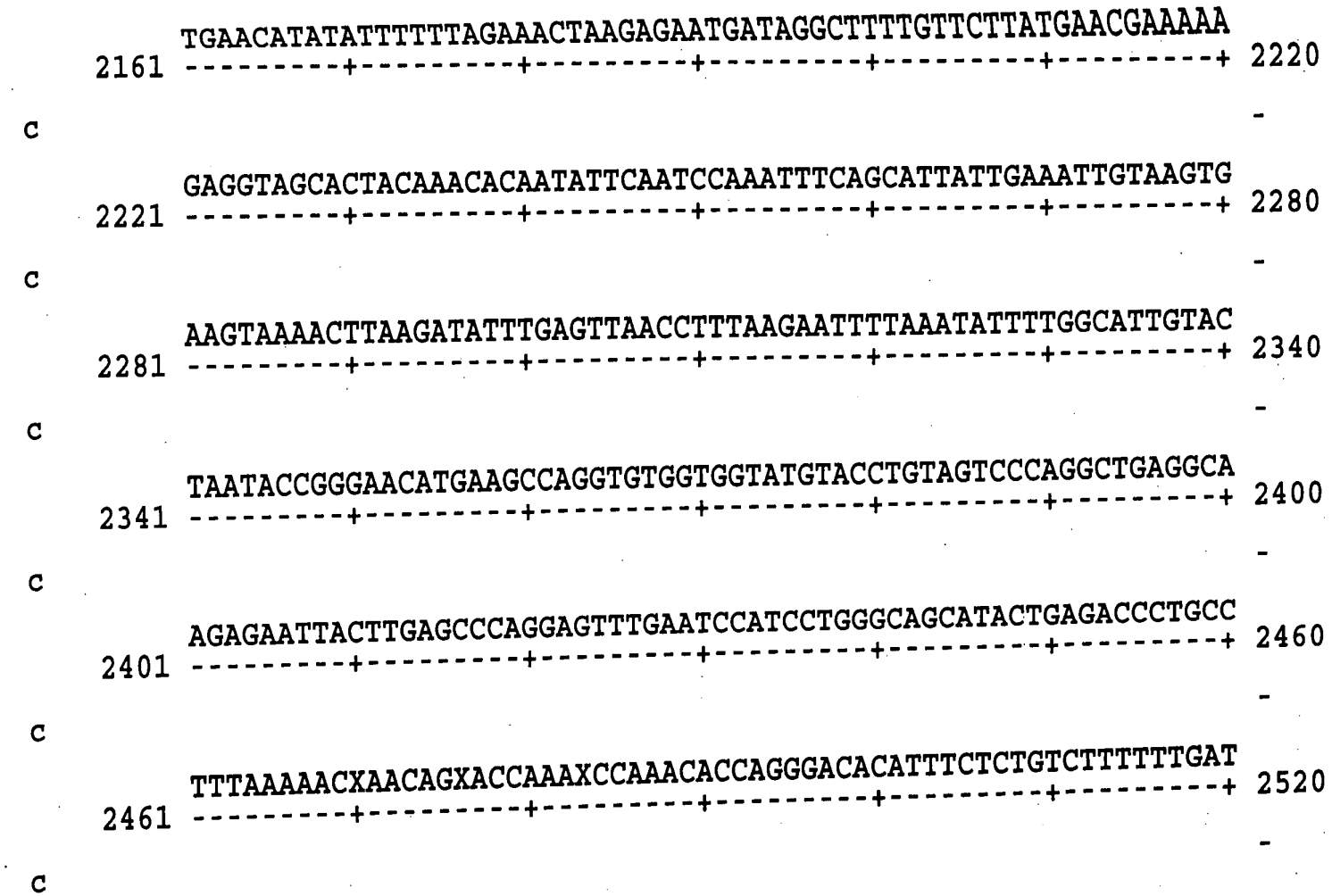

Fig. 2 (page 7 of 8)

HUMAN hiap-1

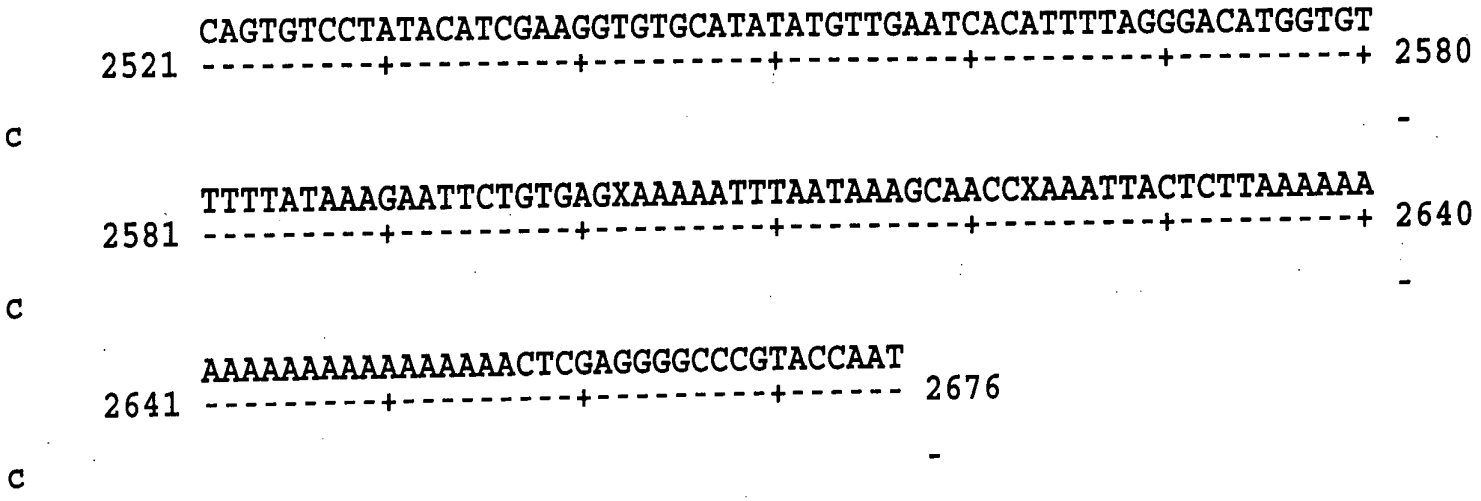

Fig. 2 (page 8 of 8)

HUMAN hiap-2

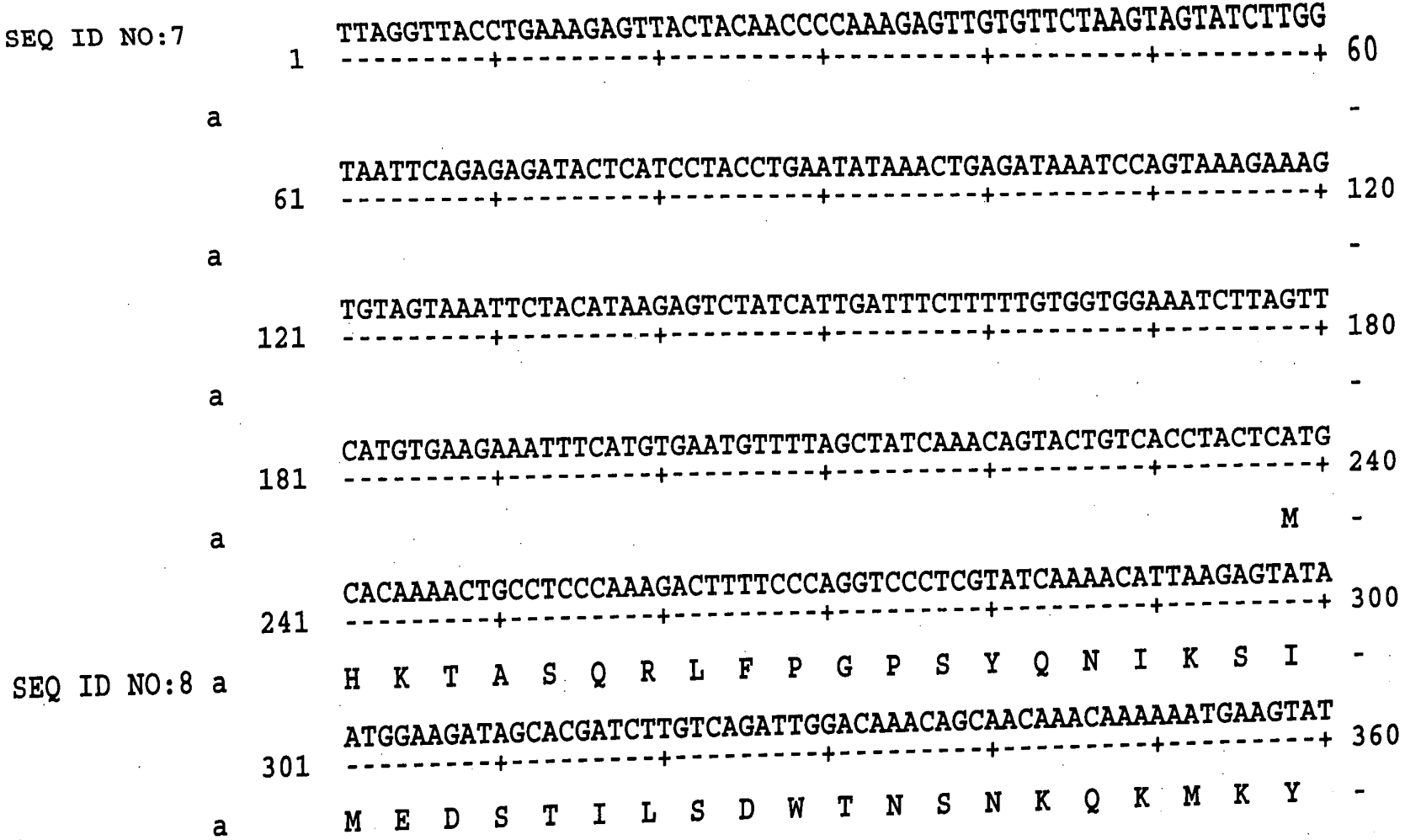

Fig. 3 (page 1 of 7)

HUMAN hiap-2

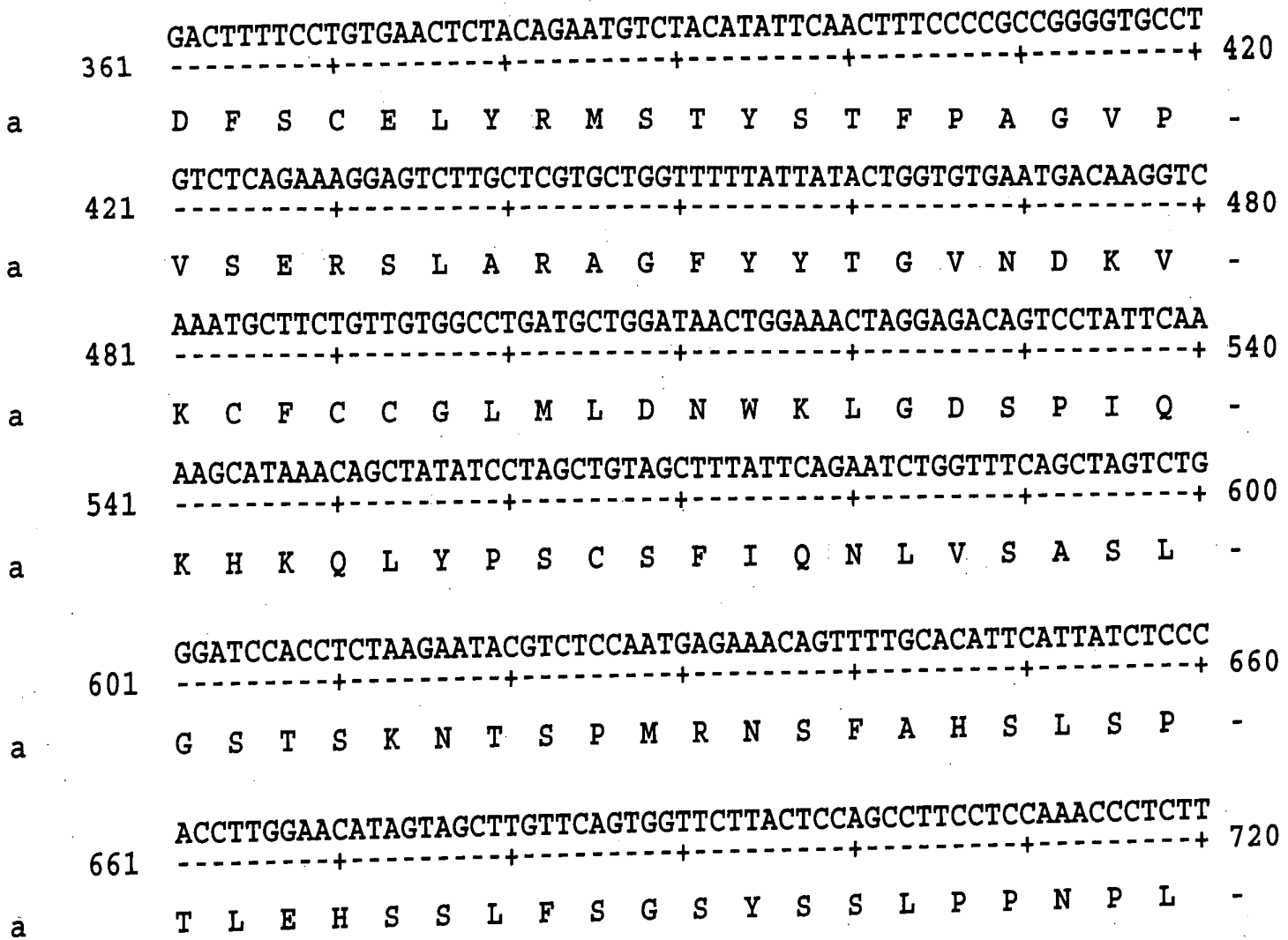

Fig. 3 (page 2 of 7)

HUMAN hiap-2

Fig. 3 (page 3 of 7)

HUMAN hiap-2

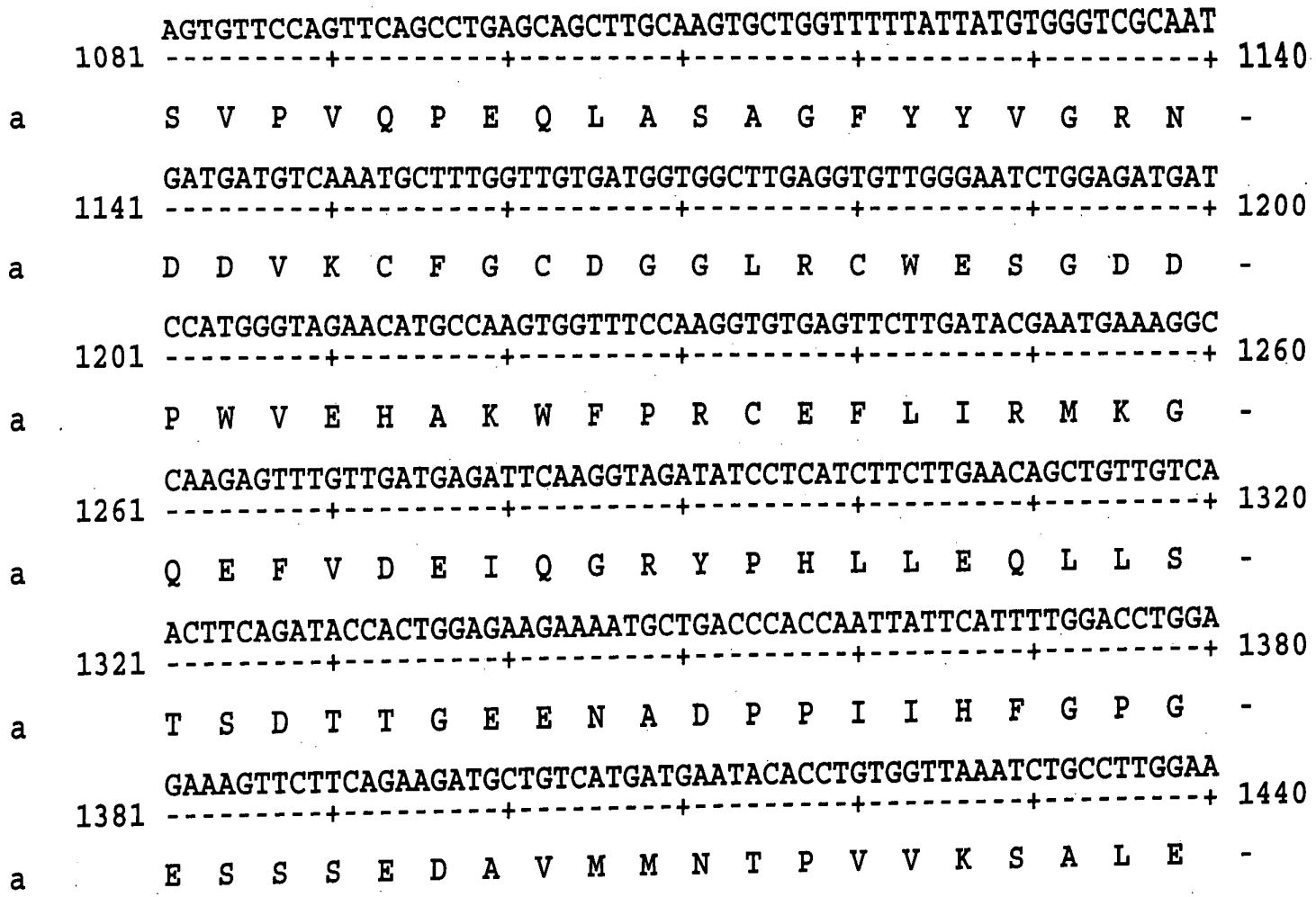

Fig. 3 (page 4 of 7)

HUMAN hiap-2

Fig. 3 (page 5 of 7)

HUMAN hiap-2

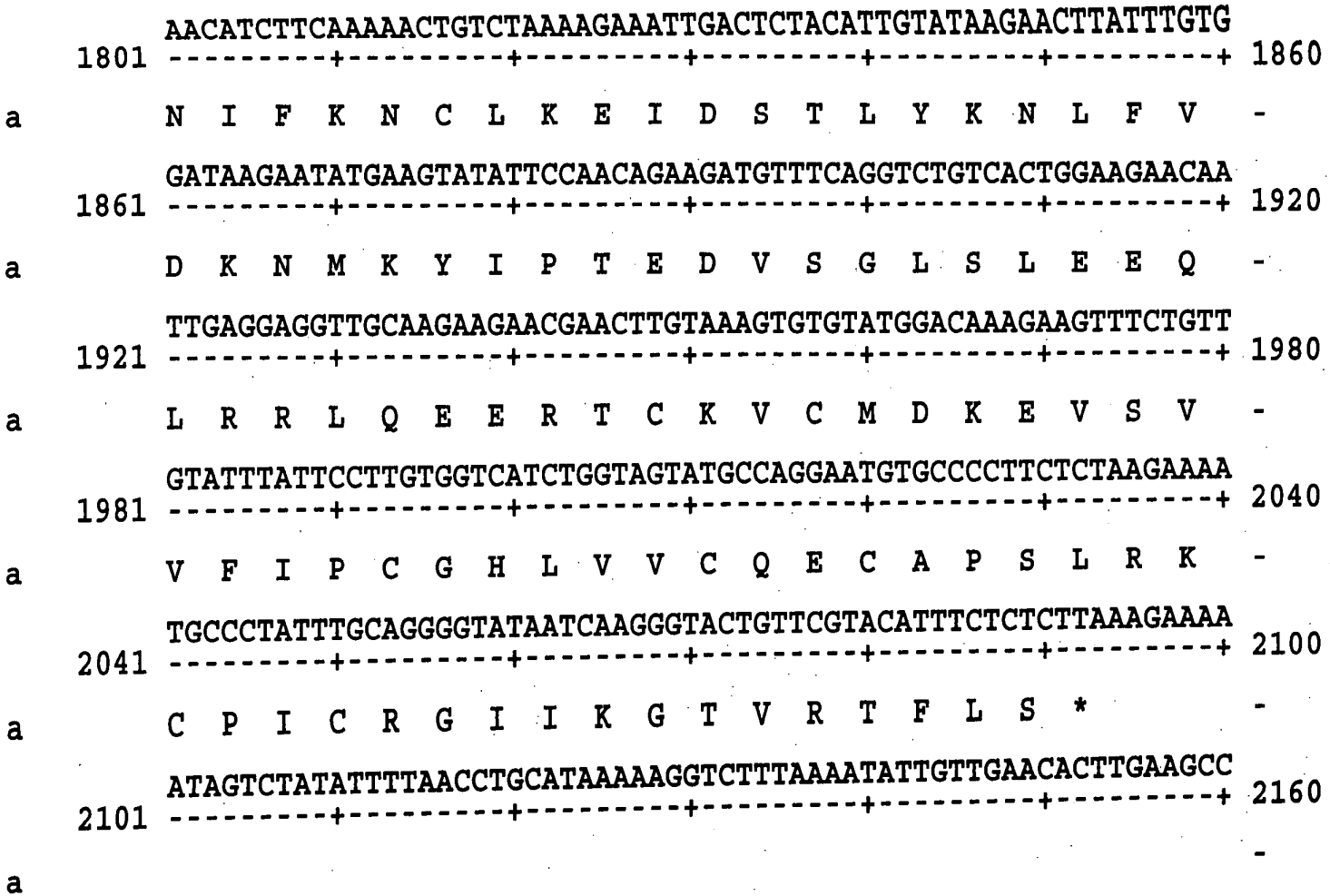

Fig. 3 (page 6 of 7)

HUMAN hiap-2

Fig. 3 (page 7 of 7)

MOUSE xiap

Fig. 4 (page 1 of 6)

MOUSE xiap

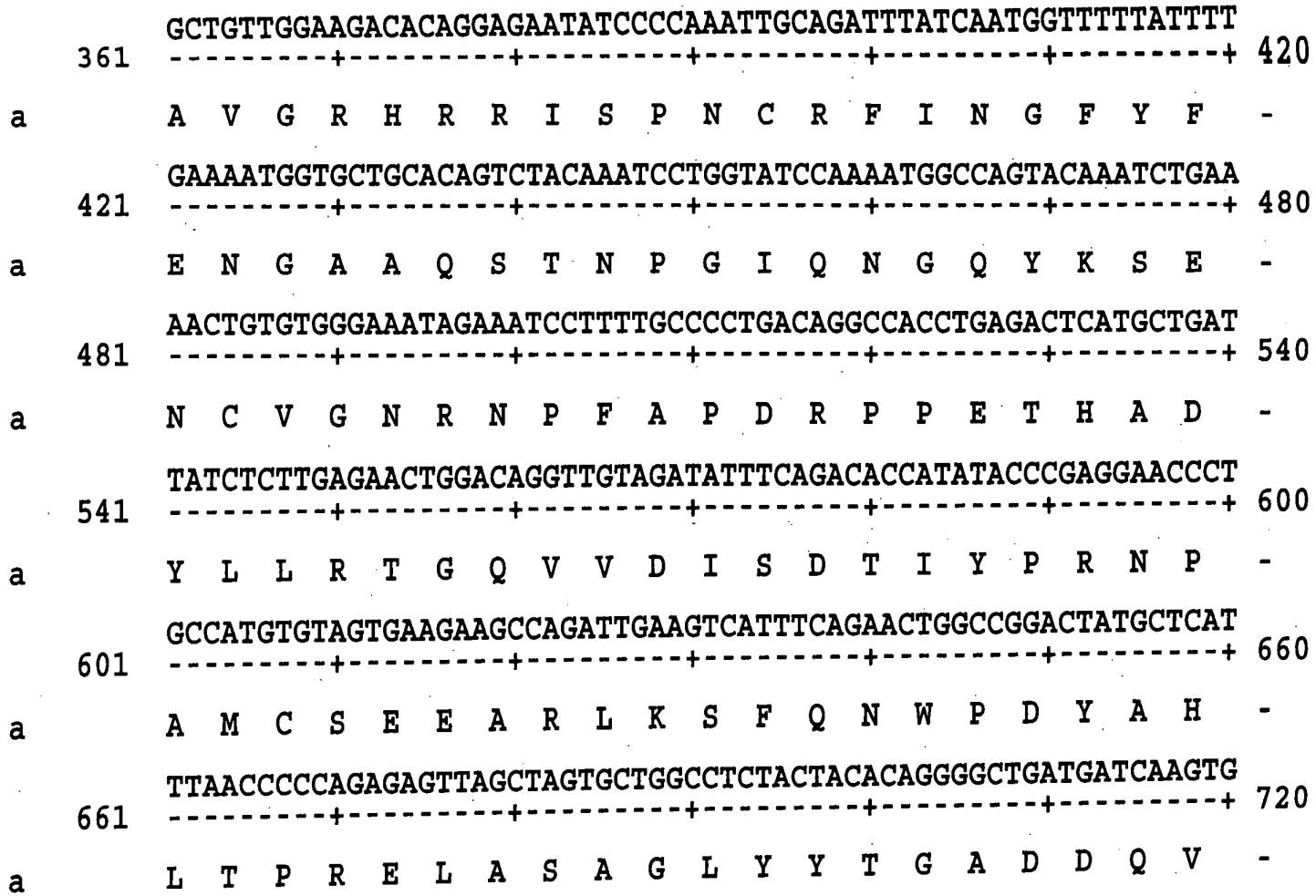

Fig. 4 (page 2 of 6)

MOUSE xiap

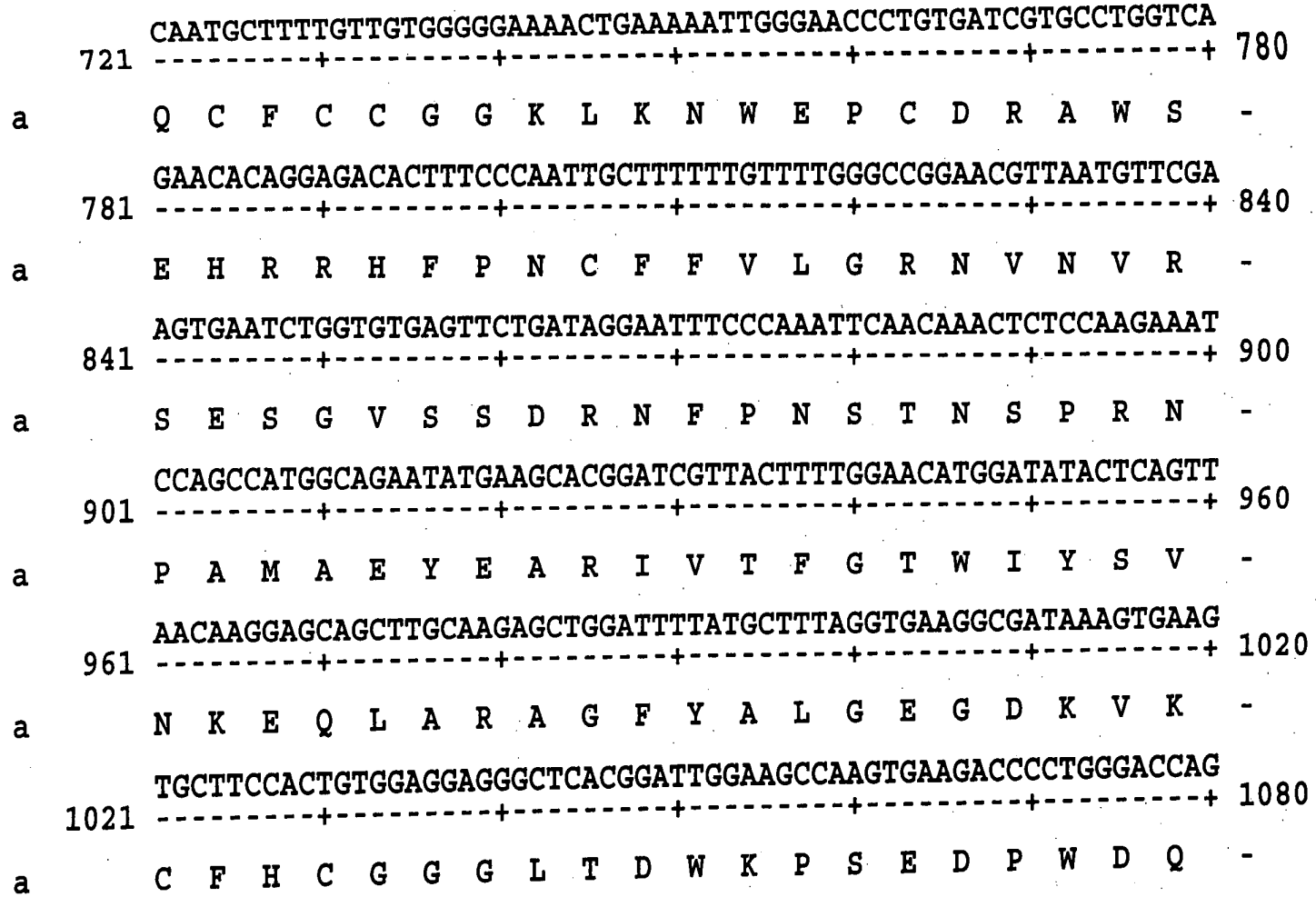

Fig. 4 (page 3 of 6)

MOUSE xiap

Fig. 4 (page 4 of 6)

MOUSE xiap

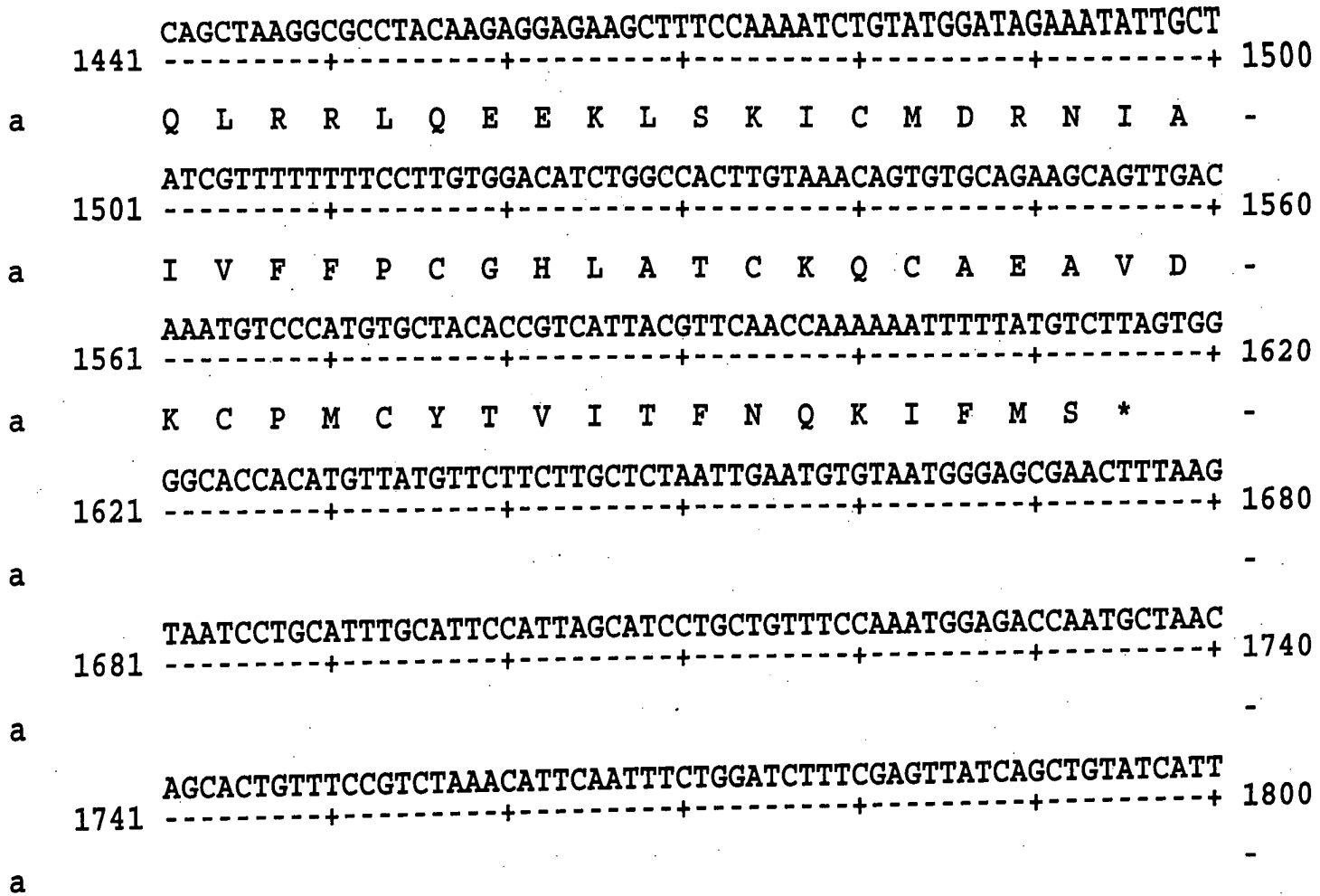

Fig. 4 (page 5 of 6)

MOUSE xiap

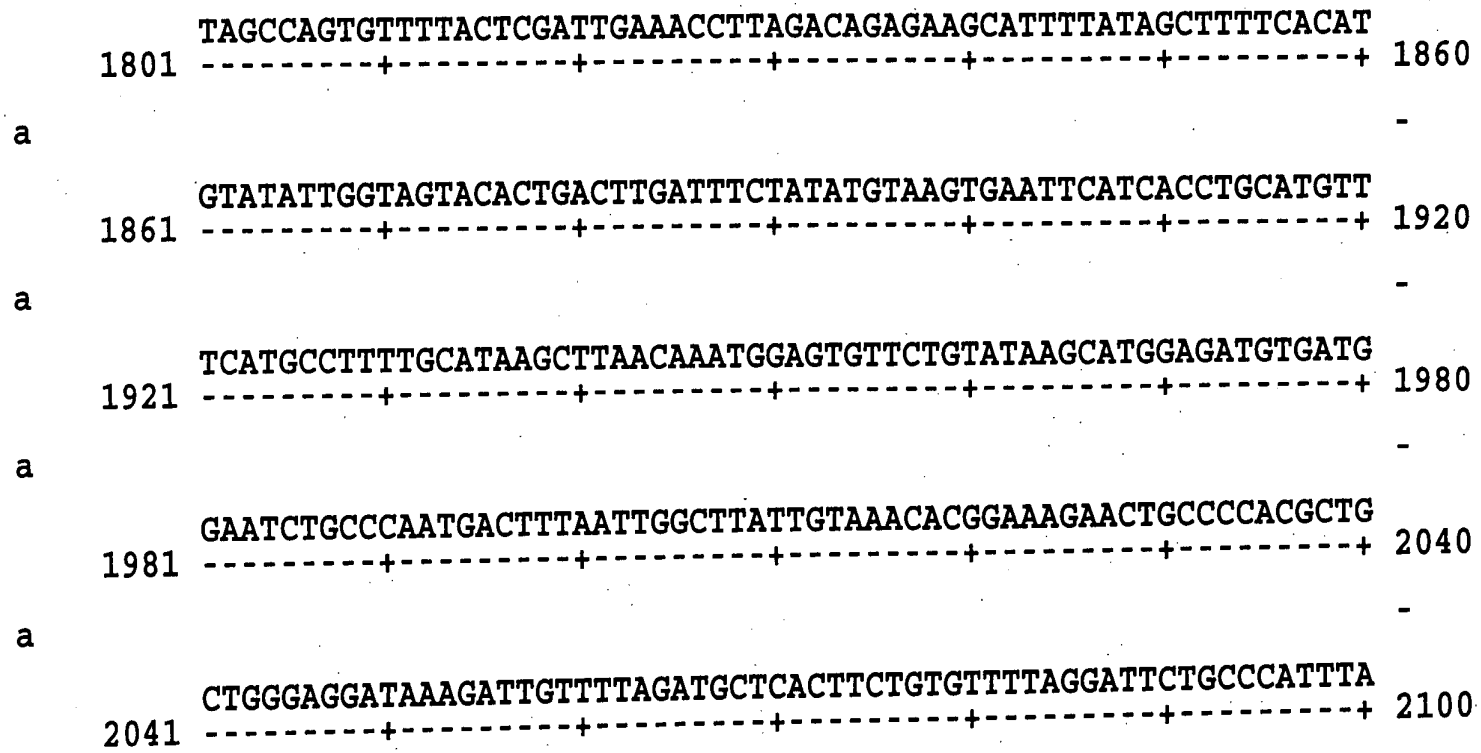

Fig. 4 (page 6 of 6)

M-hiap-1

Fig. 5 (page 1 of 6)

M-hiap-1

Fig. 5 (page 2 of 6)

M-hiap-1

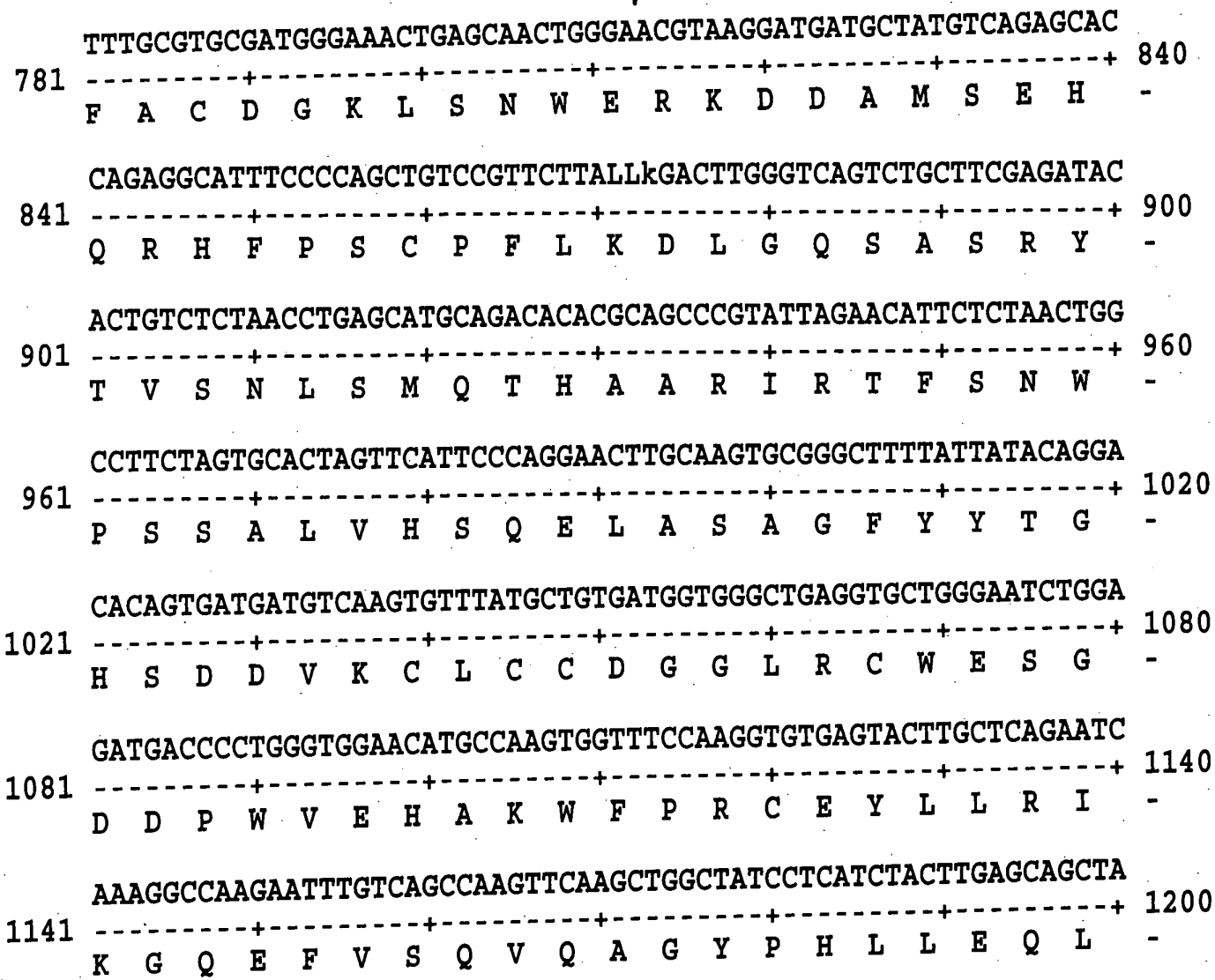

Fig. 5 (page 3 of 6)

M-hiap-1

Fig. 5 (page 4 of 6)

M-hiap-1

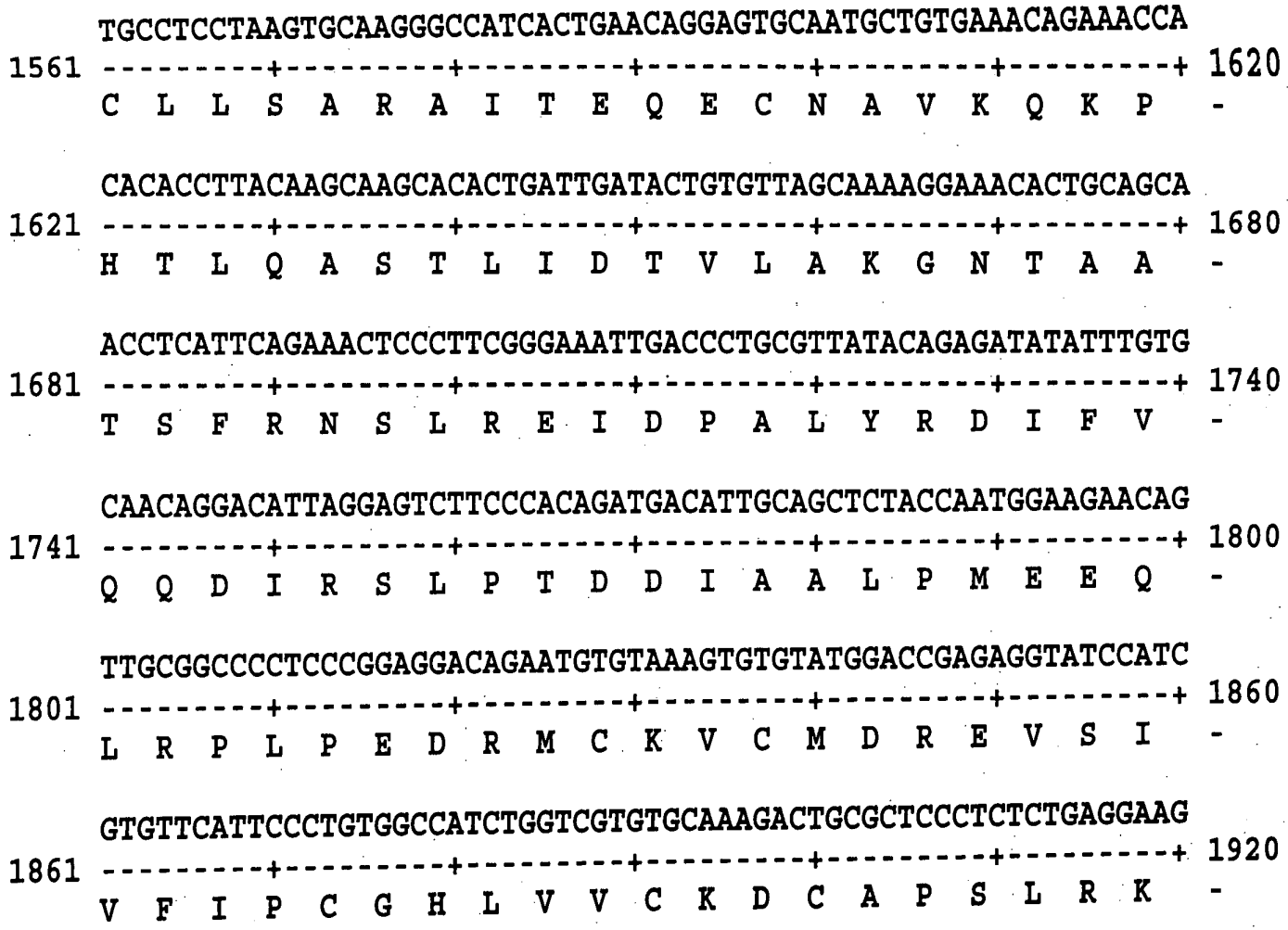

Fig. 5 (page 5 of 6)

M-hiap-1

```
     TGTCCCATCTGTAGAGGGACCATCAAGGGCACAGTGCGCACATTTCTCTCCTGAACAAGA
1921 ---------+---------+---------+---------+---------+---------+ 1980
     C  P  I  C  R  G  T  I  K  G  T  V  R  T  F  L  S  *        -

     CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACTGTCACTCCCAGTTCCAT
1981 ---------+---------+---------+---------+---------+---------+ 2040
     TCGGAACTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACkCACAAATATAAACAT
2041 ---------+---------+---------+---------+---------+---------+ 2100
     GAAAAACTTTTGTCTGAAGTCAAGAATGAATGAATTACTTATATAATAATTTTAATTGGT
2101 ---------+---------+---------+---------+---------+---------+ 2160
     TTCCTTAAAAGTGCTATTTGTTCCCAACTCAGAAAATTGTTTTCTGTAAACATATTTACA
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TACTACCTGCATCTAAAGTATTCATATATTCATATATTCAGATGTCATGAGAGAGGGTTT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TGTTCTTGTTCCTGAAAAGCTGGTTTATCATCTGATCAGCATATACTGCGCAACGGGCAG
2281 ---------+---------+---------+---------+---------+---------+ 2340
     GGCTAGAATCCATGAACCAAGCTGCAAAGATCTCACGCTAAATAAGGCGGAAAGATTTGG
2341 ---------+---------+---------+---------+---------+---------+ 2400
     AGAAACGAAAGGAAATTCTTTCCTGTCCAATGTATACTCTTCAGACTAATGACCTCTTCC
2401 ---------+---------+---------+---------+---------+---------+ 2460
     TATCAAGCCTTCTA
2461 ---------+---- 2474
```

Fig. 5 (page 6 of 6)

M-hiap-2

Fig. 6 (page 1 of 6)

M-hiap-2

Fig. 6 (page 2 of 6)

M-hiap-2

Fig. 6 (page 3 of 6)

M-hiap-2

Fig. 6 (page 4 of 6)

M-hiap-2

Fig. 6 (page 5 of 6)

M-hiap-2

```
     GAAGTGCCCCATCTGCAGGGGGACAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGT
1861 ---------+---------+---------+---------+---------+---------+ 1920
      K  C  P  I  C  R  G  T  I  K  G  T  V  R  T  F  L  S  *     -

     GAAGAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACTAC
1921 ---------+---------+---------+---------+---------+---------+ 1980
     TGATTTCAGCTCTTCAGCAGGACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTAT
1981 ---------+---------+---------+---------+---------+---------+ 2040
     GAAGGGTAGCATTGTATATTTAAGCTTAGTCTGTTGCAAGGGAAGGTCTATGCTGTTGAG
2041 ---------+---------+---------+---------+---------+---------+ 2100
     CTACAGGACTGTGTCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGA
2101 ---------+---------+---------+---------+---------+---------+ 2160
     CTTCTTGGGATTTGGGAATTTGGGGAAAGCTTTGGAATCCAGTGATGTGGAGCTCAGAAA
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TCCTGGAACCAGTGACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TCCAGTCTGGGAAATAAGGAGGAATCTGCTGCTGGTAAAAATTTGCTGGATGTGAGAAAT
2281 ---------+---------+---------+---------+---------+---------+ 2340
     AGATGAAAGTGTTTCGGGTGGGGGCGTGCATCAGTGTAGTGTGTGCAGGGATGTATGCAG
2341 ---------+---------+---------+---------+---------+---------+ 2400
     GCCAAACACTGTGTAG
2401 ---------+------ 2416
```

Fig. 6 (page 6 of 6)

Alignment of BIR (Baculoviral IAP Repeats) Domains

Baculovirus
- Cp_iap — Cydia pomonella
- Op_iap — Orgyia pseudotsugata

Human
- xiap — IAP on X chromosome
- hiap1, hiap2 — two different human IAP genes

Mouse
- m-xiap — mouse homologue of human xiap gene

Insect
- diap — Drosophilia IAP gene, not clearly a homologue of xiap or hiap

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

Fig. 7

```
                                 1                                                  68
SEQ ID NO:11   Op_iap-1    kaaRLgTYtn WPvqf.leps rMAasGFYYl GrgDeVrCaf CkveitnWvr gDdpetdHkr waPqCpFV
SEQ ID NO:14   Cp_iap-1    eevRLnTFek WPvsf.lspe tMAknGFYYl GrsDeVrCaf CkveimrWke gEdpaadHkk waPqCpFV
SEQ ID NO:15   diap-2      eanRLvTFkd WPnpn.iLpq aLAkAGFYYl nrlDhVkCvw CngviakWek nDnafeeHkr ffPqCprV
SEQ ID NO:16   m-xiap-1    efnRLkTFan FPssspvsas tLArAGFLYt GegDtVqCFs ChaaidrWqy gDsavgrHrr isPnCrFI
SEQ ID NO:17   xiap-1      efnRLkTFan FPsgspvsas tLArAGFLYt GegDtVrCFs ChaavdrWqy gDsavgrHrk vsPnCrFI
SEQ ID NO:18   hiap1-1     elyRMsTYst FPagvpvser sLArAGFYYt GvnDkVkCFc CglmldnWkr gDsptekHkk lyPsCrFV
SEQ ID NO:19   hiap2-1     elyRMsTYst FPagvpvser sLArAGFYYt GvnDkVkCFc CglmldnWkl gDspiqkHkq lyPsCsFI
SEQ ID NO:20   m-xiap-2    eeaRLksFqn WPdyahltpr eLAsAGLYYt GadDqVqCFc CggklknWep cDrawseHrr hfPnCfFv
SEQ ID NO:21   xiap-2      eeaRLksFqn WPdyahltpr eLAsAGLLYt GigDqVqCFc CggklknWep cDrawseHrr hfPnCfFV
SEQ ID NO:22   hiap1-2     enaRL1TFqt WP.lLflspt dLArAGFYYi GpgDrVaCFa CggklsnWep kDnamseHlr hfPkCpFI
SEQ ID NO:23   hiap2-2     eeaRFlTYhm WP.lLflsps eLArAGFYYi GpgDrVaCFa CggklsnWep kDdamseHrr hfPnCpFl
SEQ ID NO:24   m-xiap-3    yeaRivTFgt Wiysv..nke qLArAGFYal GegDkVkCFh CgggltdWkp sEdpwdqHak cyPgCkYl
SEQ ID NO:25   xiap-3      yeaRifTFgt Wiysv..nke qLArAGFYal GegDkVkCFh CgggltdWkp sEdpweqHak wyPgCkYl
SEQ ID NO:26   hiap1-3     haaRFkTFfn WPssvlvnpe qLAsAgFYYv GnsDdVkCFc CdgglrcWes gDdpwvqHak wfPrCeYl
SEQ ID NO:27   hiap2-3     haaRMrTFmy WPssvpvqpe qLAsAGFYYv GrnDdVkCFg CdgglrcWes gDdpwveHak wfPrCeFl
SEQ ID NO:28   Op_iap-2    eaaRLrTFae WPrglkqrpe eLAeAGFFYt GqgDktrCFc CdgglkdWep dDapwqqHar wydrCeYV
SEQ ID NO:29   Cp_iap-2    eaaRvksFhn WPrcmkqrpe qMAdAGFFYt GygDntkCFy CdgglkdWep eDvpweqHvr widrCaYV
SEQ ID NO:30   diap-3      vdaRLrTFtd WPisniqpas aLAqAGLYYq kigDqVrCFh CniglrsWqk eDepwieHak wsPkCqFV
SEQ ID NO:31   diap-1      esvRLaTFge WPlnapvsae dLvanGFF.. GtwmeaeCdf ChvridrWey gDlvaerHrr ssPiCsmV
SEQ ID NO:2    Consensus   ---RL-TF-- WP-------- -LA-AGFYY- G--D-V-CF- C------W-- -D-----H-- --P-C-FV
```

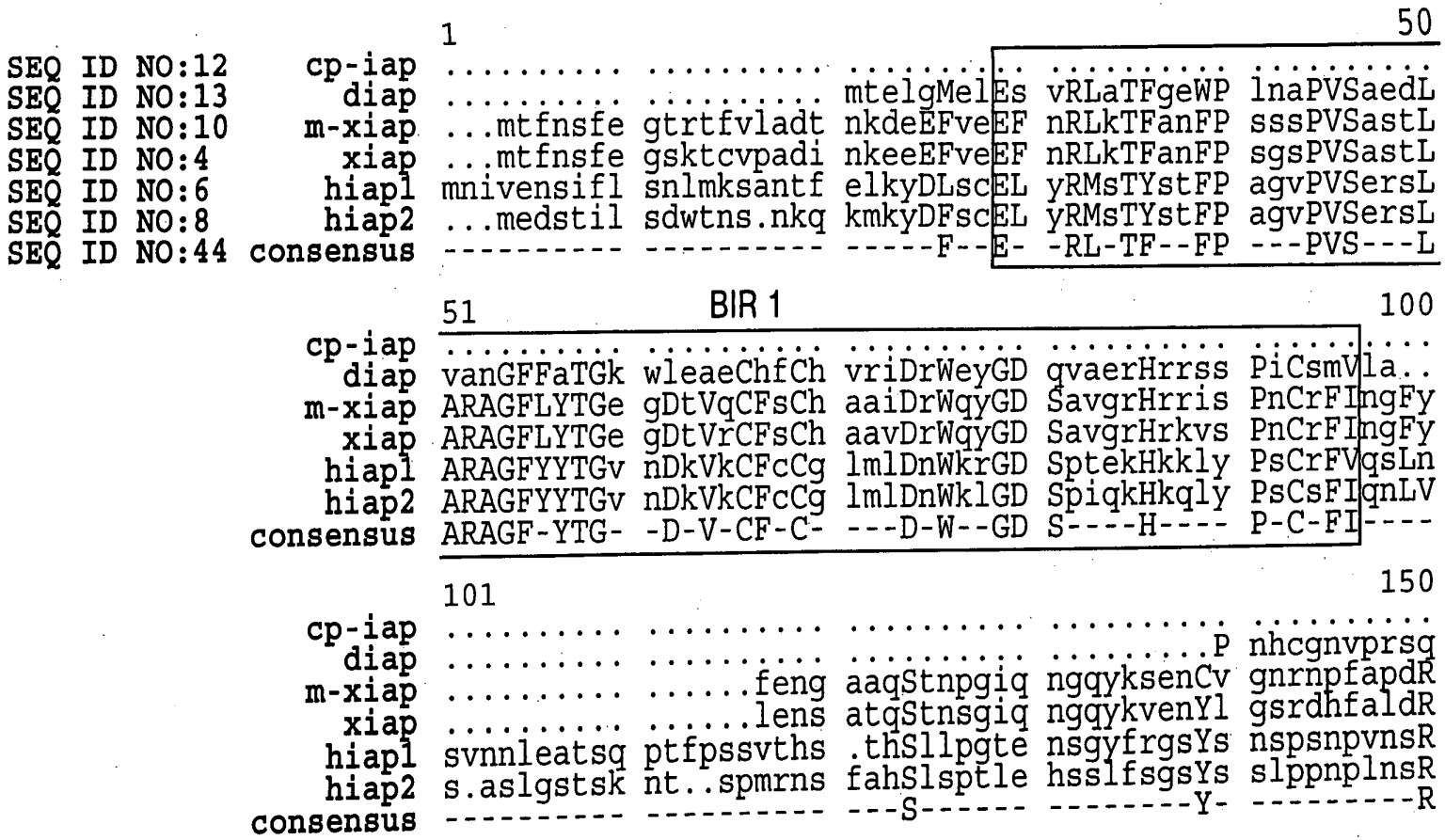

Fig. 8 (page 1 of 5)

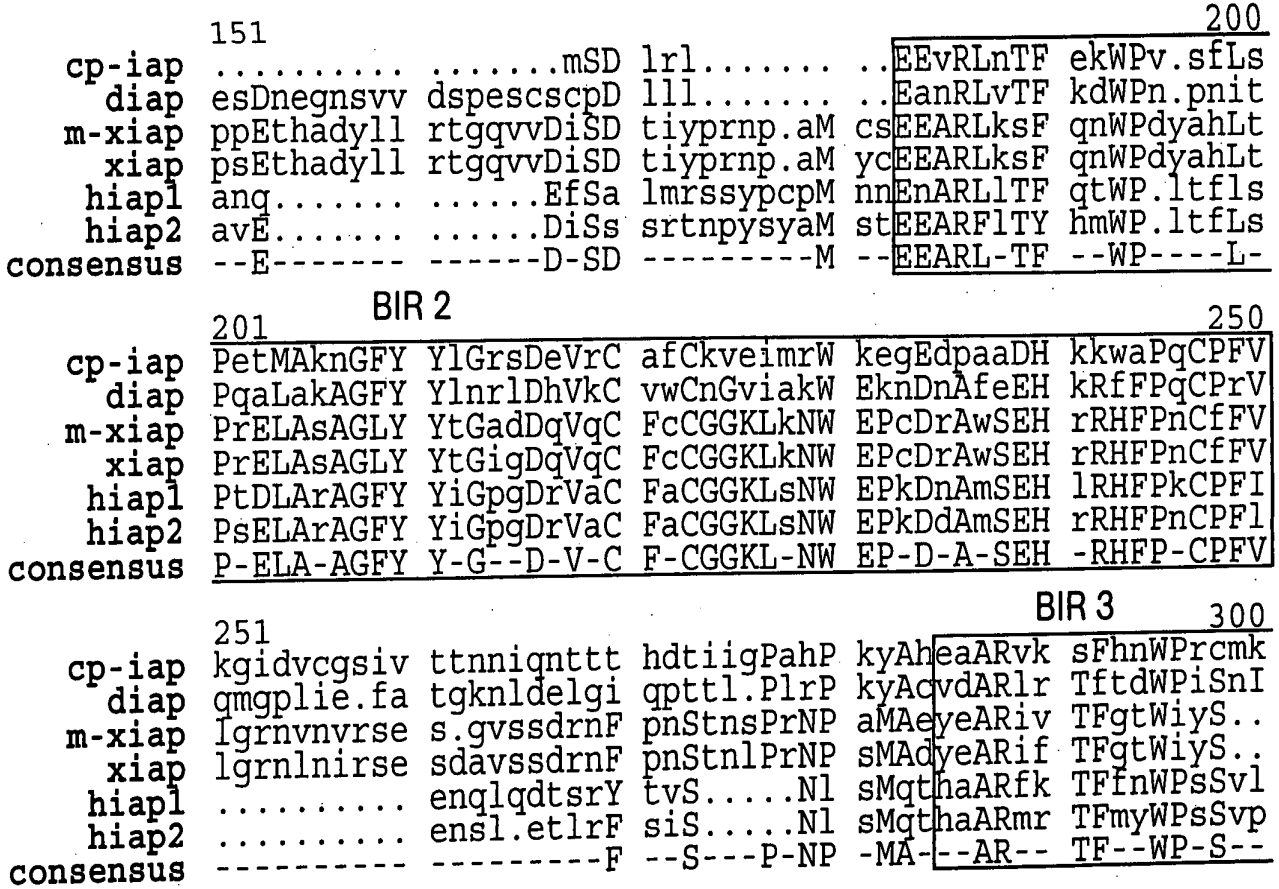

Fig. 8 (page 2 of 5)

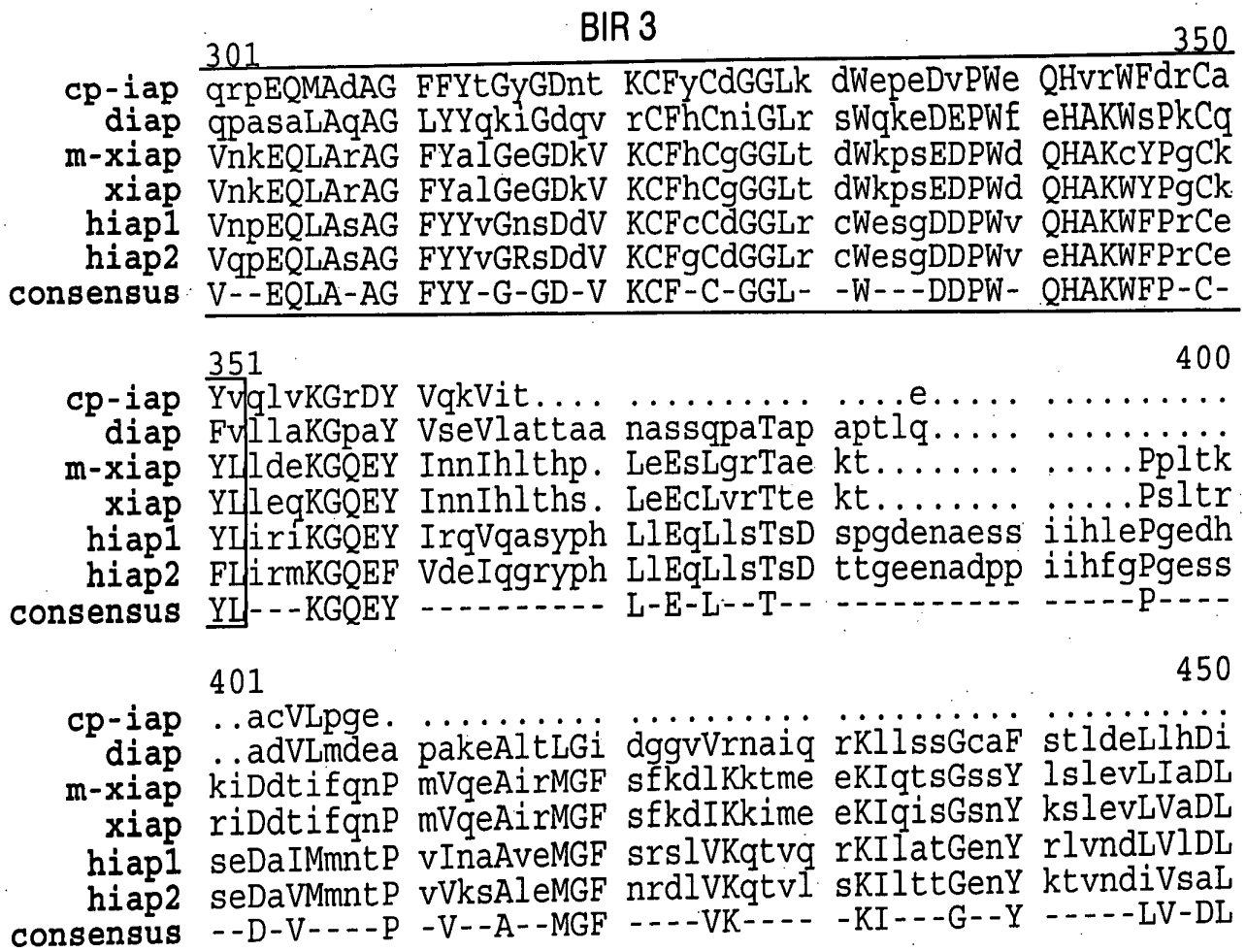

Fig. 8 (page 3 of 5)

```
           451                                                        500
cp-iap     .......... .......... .......... .......... ..........
  diap     fddagagaal Evreppe... .......... .......... ..........
m-xiap     vsAqkDnteD E......... .......... .......... ..........
  xiap     vnAqkDsmqD E......... .......... .......... ..........
 hiap1     lnAedEireE Ererateeke sndlllirkn rmalfqhltc vipildsllt
 hiap2     lnAedEkreE Ekekqaeema sddlslirkn rmalfqqltc vlpildnllk
consensus  --A------- E--------- ---------- ---------- ----------

           501                                                        550
cp-iap     .......... .......... ..nttvstaa pvsepipe.. ..........
  diap     .......... ...psapfie pcqattskaa svpipvadsi pakpqaaeav
m-xiap     .......... ....ssQtsL Q......... .......... ..........
  xiap     .......... ....ssQtsL Q......... .......... ..........
 hiap1     agiineqehd vikqktQtsL Qarelidtil vkgniaatvf rnslqeaeav
 hiap2     anvinkqehd iikqktQipL Qarelidtiw vkgnaaanif knclkeidst
consensus  ---------- ------Q--L Q--------- ---------- ----------
```

Fig. 8 (sheet 4 of 5)

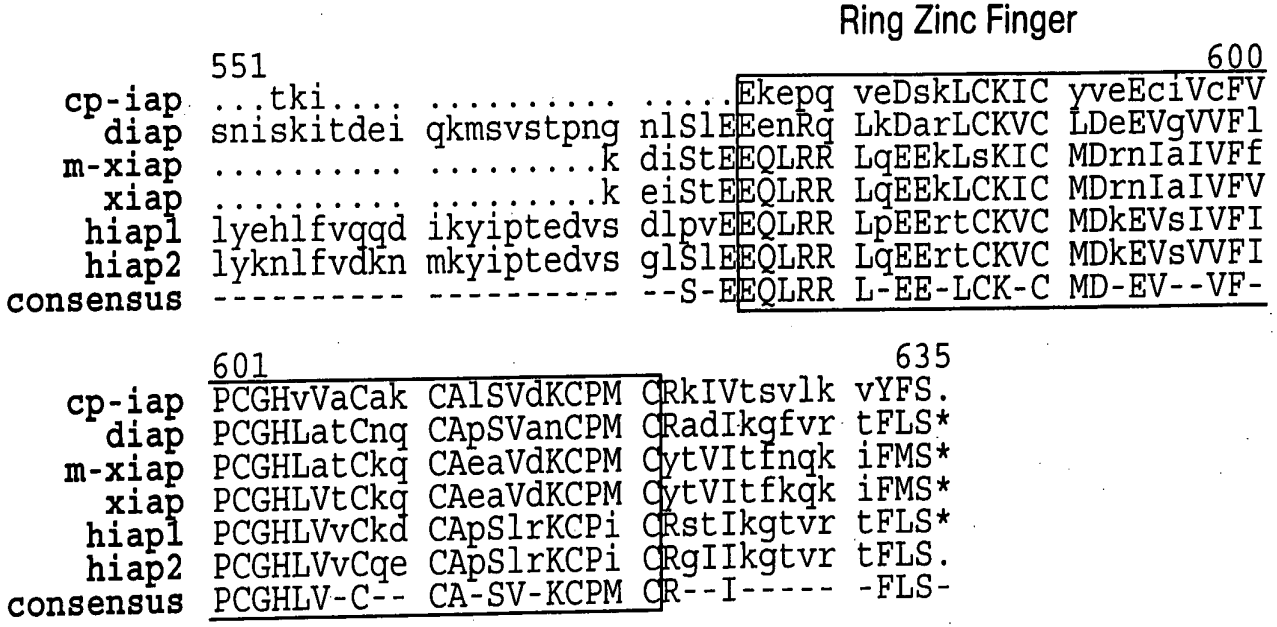

Fig. 8 (sheet 5 of 5)

Alignment of RZF (Ring Zinc Finger) Domains

Baculovirus
- Cp_iap — Cydia pomonella
- Op_iap — Orgyia pseudotsugata

Human
- xiap — IAP on X chromosome
- hiap1, hiap2 — two different human IAP genes

Mouse
- m-xiap — mouse homologue of human xiap gene

Insect
- diap — Drosophilia IAP gene, not clearly a homologue of xiap or hiap

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

```
                                1                                       46
SEQ ID NO:32 hiap2      Eqlrrlqeer tCKVCMdkev sVvFiPCGHl vvCqeCApel rkCPiC
SEQ ID NO:33 hiap1      Eqlrrlpeer tCKVCMdkev sIvFiPCGHl w CkdCApsl rkCPiC
SEQ ID NO:34 m-xiap     Eqlrrlqeek lsKICMdrni aIvFfPCGHl atCkqCAeav dkCPmC
SEQ ID NO:35 xiap       Eqlrrlqeek lCKICMdrni aIvFvPCGHl vtCkqCAeav dkCPmC
SEQ ID NO:36 diap       Eenrqlkdar lCKVCLdeev gVvFlPCGHl atCnqCApev anCPmC
SEQ ID NO:37 Cp_iap     EkepgveDsk lCKICyveec iVcFvPCGHv vaCakCAlsv dkCPmC
SEQ ID NO:38 Op_iap     aveaevaDdr lCKICLgack tVcFvPCGHv vaCgkCAagv ttCPvC
SEQ ID NO:1  consensus  E------E-- -CKICM---- -V-F-PCGH- --C--CA--- --CP-C
```

Fig. 9

Fig. 10A

Fig. 10B

Fig. 10C

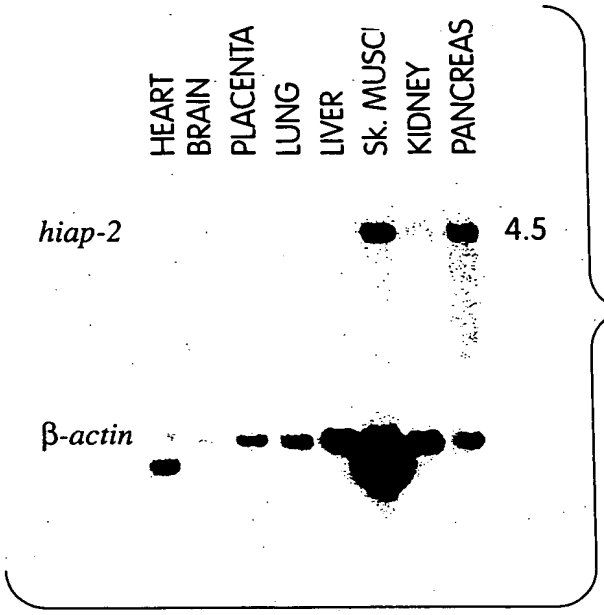

Fig. 11A

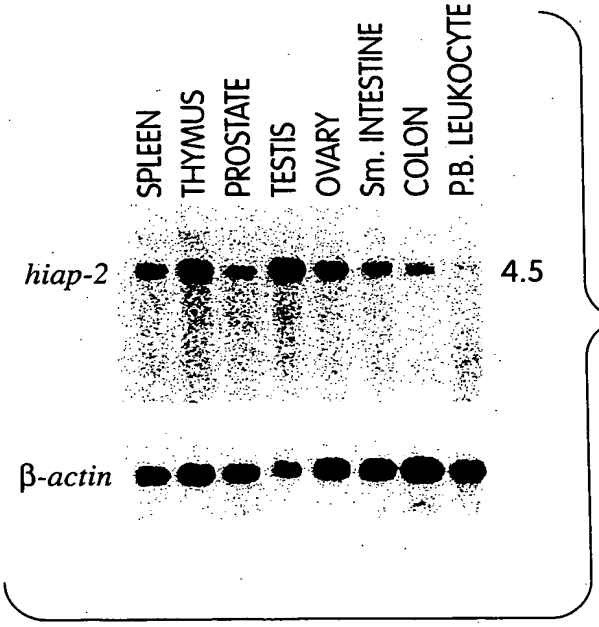

Fig. 11B

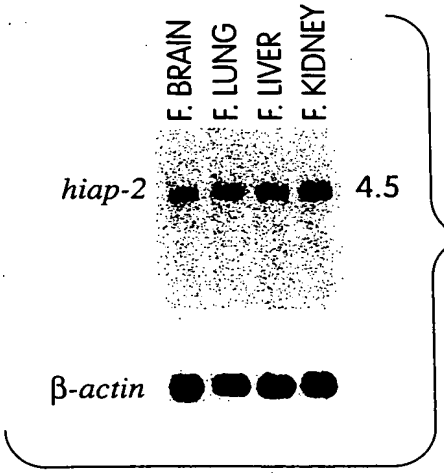

Fig. 11C

Fig. 12A

Fig. 12B

Fig. 12C

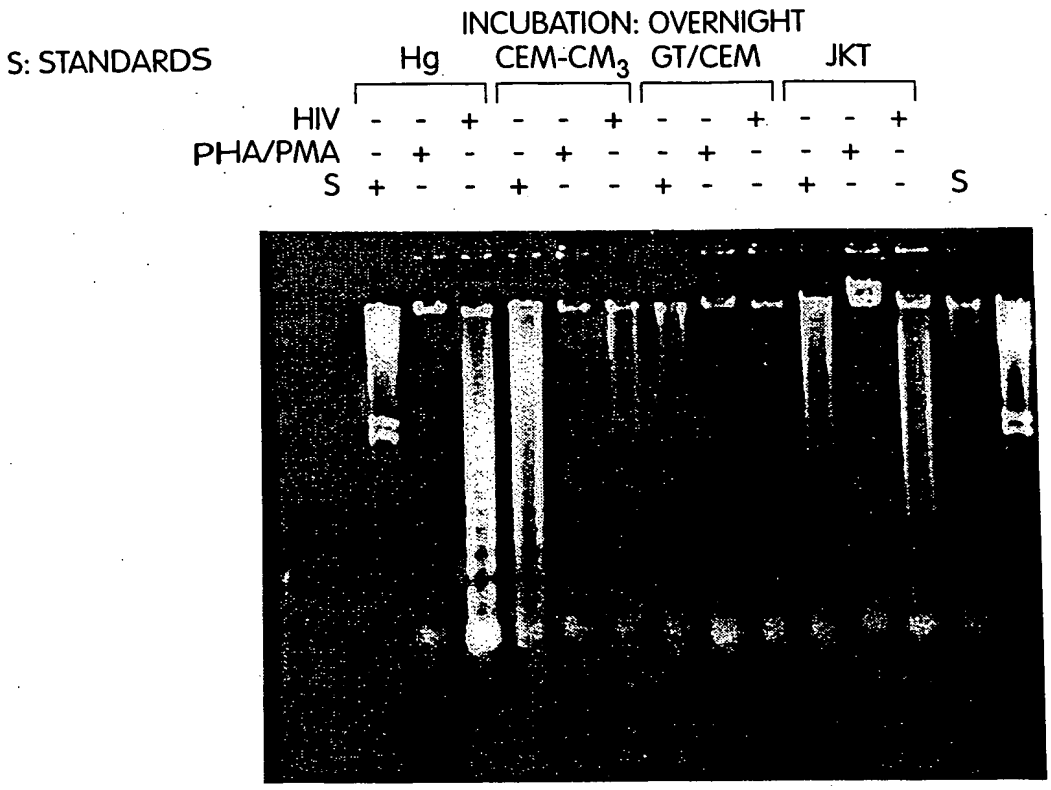

Fig. 13A

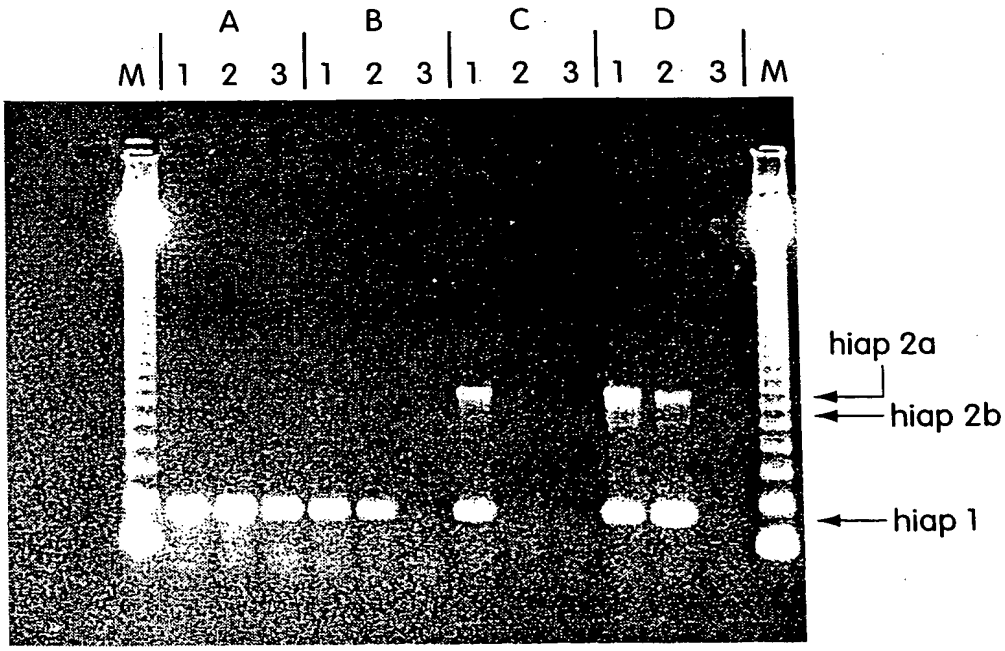

Fig. 13B

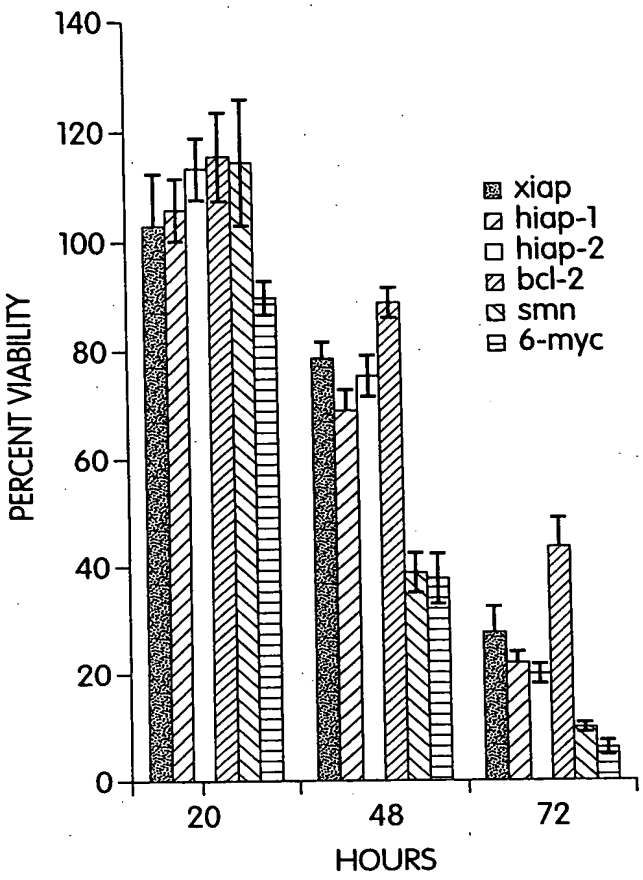

Fig. 14A

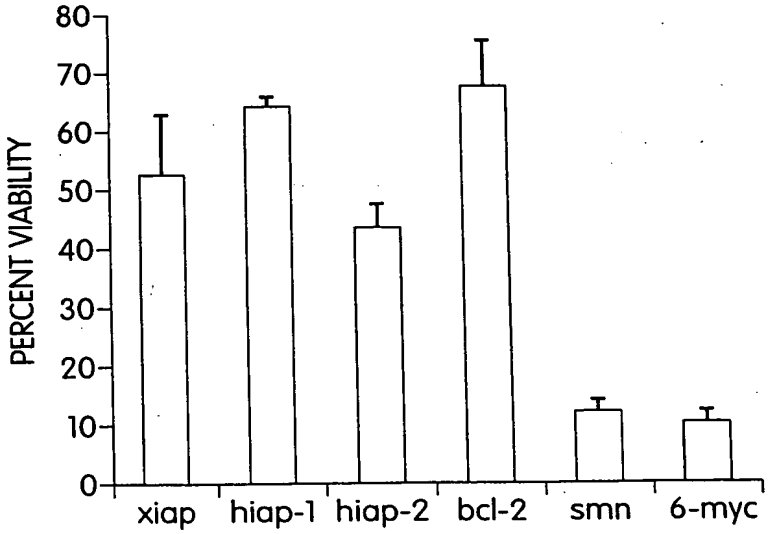

Fig. 14B

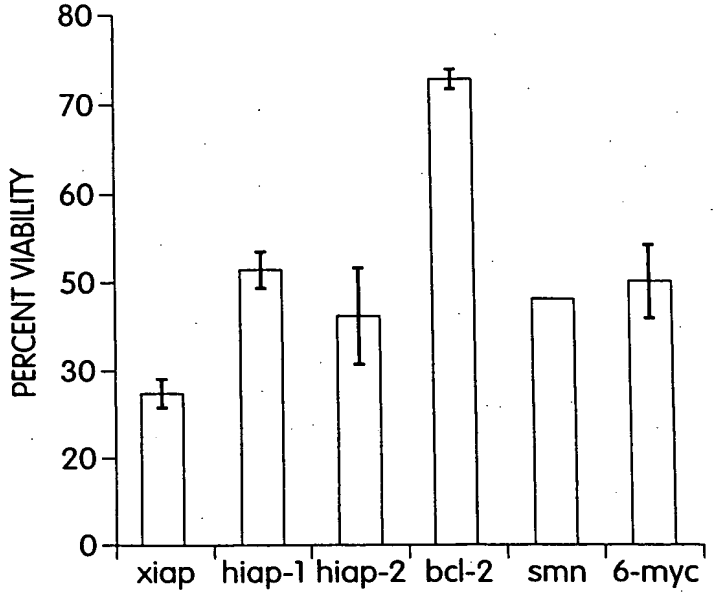

Fig. 14C

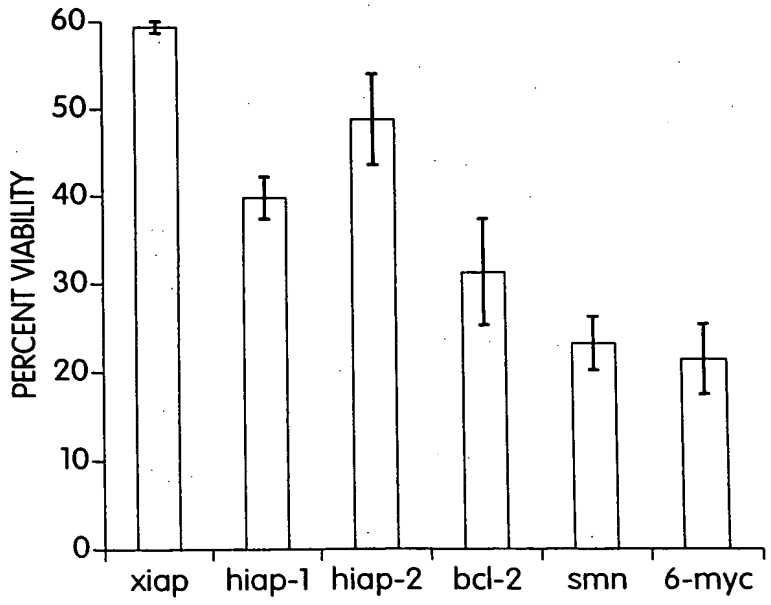

Fig. 14D